

PN *W0928471-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 25-NOV-1998; 98WO-US025270.
 XX
 PR 01-DEC-1997; 97US-0067175P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Pastan IH, Chowdhury PS;
 XX
 DR WPI; 1999-371123/31.
 XX
 N-PSDB; ABL57231.
 XX
 PT New anti-mesothelin antibodies.
 XX
 PS Claim 2; Fig 1; 63pp; English.
 XX
 CC The present sequence is the protein sequence of anti-mesothelin scFv
 CC antibody SS. This single-chain antibody was produced by immunising a
 CC mouse with cDNA encoding mesothelin, creating a phage library from mRNA
 CC isolated from the spleen of the immunised animal, and enrichment of anti-
 CC mesothelin phage over 3 rounds of panning. scFv SS is composed of a heavy
 CC chain variable region (VH) joined to a light chain variable region (VL)
 CC via a peptide linker. According to Kabat's classification, the VH belongs
 CC to sub-group IIA and family V and the VL belongs to sub-group VI and
 CC family XI. A claimed anti-mesothelin antibody binds recombinant
 CC mesothelin with a dissociation constant of less than 3 x 10 power -8 M
 CC and specifically binds to cells expressing mesothelin on their cell
 CC surface. The antibody comprises SS scFv, the VH and VL region of SS scFv
 CC or the complementarity determining regions of SS scFv. It is preferably
 CC conjugated to a therapeutic agent, particularly pseudomonas exotoxin or
 CC its cytotoxic fragment. The resulting immunconjugate is used in a
 CC claimed method for inhibiting the growth of a malignant cell that
 CC expresses mesothelin on its cell surface, especially in mesothelioma,
 CC ovarian cancer, stomach cancer or squamous cell cancer. The antibody can
 CC also be used to detect mesothelin in a biological sample
 XX
 SQ Sequence 241 AA:

Query Match 100.0%; Score 1276; DB 2; Length 241;

Best Local Similarity 100.0%; Pred. No. 1.6e-77;

Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOVQLQOSGPBELKPGASVYKLSCKASGYSTGYTMVMVKOSHGKSLIEWIGLITPPYNGASS 60
 DB 1 MOVQLQOSGPBELKPGASVYKLSCKASGYSTGYTMVMVKOSHGKSLIEWIGLITPPYNGASS 60
 QY 61 YNOKFRGKATLTIVDKSSSTAYMDLLSTSEDSAVYFCARGYDGRGFDYWGQGTITVTVSS 120
 DB 61 YNOKFRGKATLTIVDKSSSTAYMDLLSTSEDSAVYFCARGYDGRGFDYWGQGTITVTVSS 120
 QY 121 GVGSGGGGSGGGGSDIELTQSPALMSASPGKVTMTCSASSSVSYMHVYQOKSGTSPKR 180
 DB 121 GVGSGGGGSGGGGSDIELTQSPALMSASPGKVTMTCSASSSVSYMHVYQOKSGTSPKR 180
 QY 181 WIYDTSKLASGVGRFSGSGGNSYSLTISVYEAEDDATYYCOQWSGYPLTFGAGTKLEI 240
 DB 181 WIYDTSKLASGVGRFSGSGGNSYSLTISVYEAEDDATYYCOQWSGYPLTFGAGTKLEI 240
 QY 241 K 241
 DB 241 K 241

RESULT 2
 AAB50019
 ID AAB50019 standard; protein; 241 AA.
 AC AAB50019;
 XX
 DT 14-MAR-2001 (first entry)

XX Antimesothelin antibody SS single-chain Fv protein.
 DE
 XX Mesothelin; SS antibody; single-chain Fv; scFv; cytostatic;
 KM cancer therapy; ovarian cancer; mesothelioma.
 XX
 OS Unidentified.
 XX
 PN W020007346-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 26-MAY-2000; 2000WO-US014829.
 XX
 PR 27-MAY-1999; 99US-0160071P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Pastan I, Chowdhury PS;
 XX
 DR WPI; 2001-061517/07.
 XX
 PT Novel polypeptides comprising mutated antimesothelin antibody heavy or
 PT light chain variable region, having greater binding affinity for the
 XX antigen, useful as diagnostic and therapeutic agents for ovarian cancers.
 XX
 PS Disclosure; Fig 1; 70pp; English.
 XX
 CC The present sequence is antimesothelin antibody SS single chain Fv
 CC protein. This sequence was used to generate mutant antibody heavy or
 CC light chain variable regions, which have 5 times higher binding affinity
 CC for mesothelin antigen than the parental antibody (the present sequence).
 CC The mutant proteins of the present invention have substitution(s) in the
 CC complementarity determining region (CDR). Malignant cells express
 CC mesothelin on their surfaces, and so the mutant proteins of the present
 CC invention can be used to target immunotoxin to cells expressing
 CC mesothelin on their surface i.e. malignant cells. The mutant proteins of
 CC the present invention can therefore be used to treat ovarian cancers,
 CC mesotheliomas, and several other types of human cancers in which the
 CC cells bear the mesothelin antigen
 XX
 SQ Sequence 241 AA:

Query Match 100.0%; Score 1276; DB 4; Length 241;

Best Local Similarity 100.0%; Pred. No. 1.6e-77;

Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOVQLQOSGPBELKPGASVYKLSCKASGYSTGYTMVMVKOSHGKSLIEWIGLITPPYNGASS 60
 DB 1 MOVQLQOSGPBELKPGASVYKLSCKASGYSTGYTMVMVKOSHGKSLIEWIGLITPPYNGASS 60
 QY 61 YNOKFRGKATLTIVDKSSSTAYMDLLSTSEDSAVYFCARGYDGRGFDYWGQGTITVTVSS 120
 DB 61 YNOKFRGKATLTIVDKSSSTAYMDLLSTSEDSAVYFCARGYDGRGFDYWGQGTITVTVSS 120
 QY 121 GVGSGGGGSGGGGSDIELTQSPALMSASPGKVTMTCSASSSVSYMHVYQOKSGTSPKR 180
 DB 121 GVGSGGGGSGGGGSDIELTQSPALMSASPGKVTMTCSASSSVSYMHVYQOKSGTSPKR 180
 QY 181 WIYDTSKLASGVGRFSGSGGNSYSLTISVYEAEDDATYYCOQWSGYPLTFGAGTKLEI 240
 DB 181 WIYDTSKLASGVGRFSGSGGNSYSLTISVYEAEDDATYYCOQWSGYPLTFGAGTKLEI 240
 QY 241 K 241
 DB 241 K 241

RESULT 3
 ABR62132
 ID ABR62132 standard; protein; 242 AA.
 AC ABR62132;
 XX

RESULT 4

ID ADT91209 standard; protein: 242 AA.

XX AC ADT91209;

XX DT 16-DEC-2004 (first entry)

DE Single chain variable fragment (scFv) antibody #2.

XX Tumour; benign intracranial meningioma; arteriovenous malformation;
KV angiodioma; macular degeneration; melanoma; adenocarcinoma;
KW malignant glioma; prostatic carcinoma; kidney carcinoma;
KV bladder carcinoma; pancreatic carcinoma; thyroid carcinoma;
KM lung carcinoma; colon carcinoma; rectal carcinoma; brain carcinoma;
KW liver carcinoma; breast carcinoma; ovary carcinoma; angiolipoma;
RV retrolental fibroplasia; haemangioma; Kaposi's sarcoma;
single chain variable fragment; scFv; antibody.

XX Unidentified.

OS US2004191249-A1.

PV 30-SEP-2004.

PD 20-OCT-2003; 2003US-00689006.

PF 28-APR-2000; 2000WO-US011485.
PR 09-NOV-2001; 2001US-00914605.
PR 27-SEP-2002; 2002US-00259087.

PA (UYVA-) UNIV VANDERBILT.

XX Hallahan DE, Mernaugh R;
P1 WPI; 2004-698661/68.
DR N-PDB; ADT91208.

PT Screening phage-displayed antibodies binding to radiation-inducible
neantigen on cell, comprising contacting cell with antibodies, treating
cell with radiation, contacting cell with antibodies not binding to cell,
detecting bound antibody.

PS Claim 4; SEQ ID NO 20; 64pp; English.

CC The invention relates to a method for screening phage-displayed
antibodies binding to radiation-inducible neantigen on cell. The method
involves contacting cell with antibodies, treating cell with radiation,
contacting cell with antibodies not binding to cell and detecting the
bound antibody. The method is useful for screening several phages
displayed antibodies for an ability to bind to a radiation-inducible
neantigen present on a cell, where the cell is tumour cell chosen from
benign intracranial meningiomas, arteriovenous malformation, angioma,
macular degeneration, melanoma, adenocarcinoma, malignant glioma,
prostatic carcinoma, kidney carcinoma, bladder carcinoma, pancreatic
carcinoma, thyroid carcinoma, lung carcinoma, colon carcinoma, rectal
carcinoma, brain carcinoma, liver carcinoma, breast carcinoma, ovary
carcinoma, solid tumours, solid tumour metastases, angiolipomas,
retrolental fibroplasias, haemangiomias, Kaposi's sarcoma, head and neck
carcinomias and their combinations or vascular endothelial cell. The
present sequence is a single chain variable fragment (scFv) antibody that
binds to radiation-inducible neantigens.

SQ Sequence 242 AA:

Query Match 80.4%; Score 1025.5; DB 8; Length 242;
Best Local Similarity 81.7%; Pred. No. 8,4e-61;
Matches 196; Conservative 13; Mismatches 30; Indels 1; Gaps 1,

2 QVVLOGSGPELEKRGASVKLSCKRASGYSPFGYITAMWKKSHGLSEMTIGLTPPNAGSSY 61
::|::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
3 QVTKQGSGPELVKRGASVTNKSCKRSGYTFTSYVMHWKVRGGQLSMVIIGYINPYNDGRY 62
::|::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy	6	NOKEPRKATLTVDKSSSTAYMDLLSTSPDSAVVYCARGGYDGRFPDVGQGTIVTVSSG	121
Dd	63	NEFKRKAALTIDKSSSTAYMELSLTSDSAVYICAFPGVYG-ALDYGQGTIVTVSSG	121
Qy	122	VGGSGGGGGSGGGSDIELTQSPAINASAPGEKVTITCSASSSVSYMHVYQCKSGTSPRW	181
Dd	122	GGSGGGGGSGGGSDIELTQSPAINASAPGEKVTITCSASSSVSYMHVYQCKSGTSPRW	181
Qy	182	IYDTSTKLASGVPERFEFGSSGNSYSLTITSSVAEDDARTYVCCQMSGVPLTFGACTKLEIK	241
Dd	182	IYGTSMLASGVPERFSGSGSGTSTSLTITSSWEADDAATYVCCQMSGVPLTFGGGTCKLEIK	241
RESULT 5			
AA847111	ID	AA847111 standard; protein; 239 AA.	
AA847111	AC		
AA847111	DE		
DT	04-JUN-2001	(first entry)	
DE	scFv 508F.		
XX			
XX	Human; prion protein; plaque forming disease; display vehicle; kuru;		
KW	aggregating protein; amyloid plaque; brain; early onset; senility;		
KW	Alzheimer's disease; late onset; pre-symptomatic; SAA amyloidosis;		
KW	hereditary Icelandic syndrome; multiple myeloma; scrapie; BSE; CJD;		
KW	bovine spongiform encephalopathy; Creutzfeldt-Jakob Disease; FFI;		
KW	Gerstmann-Strausler-Scheinker Disease; GSS; fatal familial insomnia;		
antibody.			
XX			
OS	Synthetic.		
XX			
XX	Key	Location/Qualifiers	
FT	Domain	1..120	
FT		/note="Heavy chain"	
FT	Region	31..35	
FT		/label= CDR1	
FT	Region	50..66	
FT		/label= CDR2	
FT	Region	99..107	
FT		/label= CDR3	
FT	Peptide	121..133	
FT		/note="Linker"	
FT	Domain	134..239	
FT		/note="light chain"	
FT	Region	157..166	
FT		/label= CDR1	
FT	Region	182..188	
FT		/label= CDR2	
FT	Region	221..229	
FT		/label= CDR3	
XX			
XX	WO200118169-A2.		
XX			
PD	15-MAR-2001.		
XX			
PF	31-AUG-2000; 2000MO-IL000518.		
XX			
XX	03-SEP-1999; 99US-0152417P.		
PR	29-DEC-1999; 99US-00473653.		
PR	31-JUL-2000; 2000US-00629971.		
XX			
PA	(UTRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.		
XX			
XX	Solomon B, Frenkel D, Hanan E;		
PI			
XX	WPI: 2001-244564/25.		
DR	N-PSDB; AAC65539.		
XX			
XT	Treating amyloidogenic disease such as Alzheimer's disease, BSE or CJD		
FT	comprises presentation of plaque derived antigens or epitopes on a		

PT display vehicle, and introducing the vehicle into the recipient.
 PS
 PX
 XX Example 2; Fig 11; 120pp; English.
 CC This sequence shows scFv 508F heavy chain, linker and light chain. The
 CC scFv fragment was derived from the 508 IgM hybridoma which is generated
 CC from splenocytes of a mouse that has been immunised with a peptide
 CC corresponding to the 16 amino terminal residues of beta-A β conjugated to
 CC keyhole limpet haemocyanin used a carrier. The resultant variable chain
 CC fragments may be used in the method of the invention. Cys 96 of the VL
 CC fragment was replaced with various amino acids to see if production yield
 CC or stability were effected without having an adverse effect on its
 CC binding affinity. The invention provides an agent for treating a plaque
 CC forming disease. Antigenic polypeptides are displayed on a display
 CC vehicle and are capable of eliciting antibodies capable of disaggregating
 CC the aggregating protein and/or of preventing aggregation of the
 CC aggregating protein. This reduces formation of amyloid plaques in the
 CC brain of victims of plaque forming diseases, e.g. early onset Alzheimer's
 CC disease, late onset Alzheimer's disease, pre-symptomatic Alzheimer's
 CC disease, SAA amyloidosis, hereditary Icelandic syndrome, senility,
 CC multiple myeloma, scrapie, bovine spongiform encephalopathy (BSE), kuru,
 CC Creutzfeldt-Jakob Disease (CJD), Gerstmann-Strausler-Sheinker Disease
 CC (GSS) and fatal Familial Insomnia (FFI)

SQ Sequence 239 AA;

Query Match	79.2%	Score 1010.5	DB 4	Length 239
Best Local Similarity	79.8%	Pred. No. 8.3e-60		
Matches 194	Conservative 16	Mismatches 26	Indels 7	Gaps 2

```
Qy      2 QVQLDSSGPELEKPGASVKLSCKASGYSTFTGMNWNVKSHGSLEWIGITPTPYNGASSY 61
        |||::|||:|||||::|:|||||::|:|:|
Db      1 QVKLGSGAELVRPGSVKISKCSGYTFTDYAMHWNVQSHAKSLEWICVISTSYGGDASY 60
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Oy      62 NOKFRKATLTVDKSSSTAYMDLSLTSEDSAVYFCARG--GYDGRGEDIWGOCTTVV 11
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      61 NOKFKRKATMIVDKSSSTAYMELARLTSEDSATYYCARGATMSY----FDYWGOQTVTV 11
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QY      119 SSGVGSGGGGCGGGSDIELTQSPALMSASPEKVTWTCSSASSVSYNHWYQQKSGTSP 17
        ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
Db      117 SSGGGSGGVSSGGGSDIELTQSPALMSASPEKVTWTCSSASSISYNHWYQQKRGTSR 17
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Qy 179 KRMIYDTSKLASGVPGRFSGSSGNSYSLTTSIVEAEDDATYYCQQMSGYPLTFEAGTKL 23
      |||||
Db 177 KRMIYDTSKLASGVPARFSGSSGTSYSLTTSIMEAEDATYYCHQRSSYPTTFGGAKL 23
      |||||
```

Qy	239	EIK	241
Db	237	EIK	239

RESULT 6
AA016066
ID AA016066 standard; protein; 239 AA

AC	AA016066;
XX	
DT	27-FEB-2003 (first entry)

DE	Human neurological/CNS disease treatment method-related protein.
XX	
KM	Vaccine; gene therapy; neurological disease; CNS disorder;
KM	central nervous system disorder; olfactory system; Alzheimer's disease
KM	Creutzfeldt-Jakob disease; Huntington's chorea; Parkinson's disease;
KM	viral infection of the brain; brain tumour; lysosomal storage disease;
KM	multiple sclerosis.

OS Homo sapiens.

PN WO200274243-A2.

PD 26-SEP-2002.

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PF 15-MAR-2002; 2002WO-US008042.
XX
XX 15-MAR-2001; 2001US-00808037.
XX
XX (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.
PA (MCIN/) MCINNIS P.
PI Solomon B, Frenkel D;
XX
XX WPI, 2003-040542/03.
DR N-PSDB; AAL51099.
XX
XX Treating or diagnosing neurological diseases of the central nervous
PT system, e.g. Alzheimer's disease, comprises displaying a polypeptide or
PT diagnostic agent on viral display vehicle and introducing or detecting
PT the display vehicle.
XX
XX Example 2; Fig 11A; 214pp; English.
XX
XX The invention comprises a method for treating a neurological disease or a
CC central nervous system (CNS) disorder. The method involves displaying a
CC therapeutic molecule capable of treating the neurological disease or CNS
CC disorder on a viral display vehicle. The viral display vehicle is then
CC introduced into the olfactory system of a subject to treat the disease or
CC disorder. The method of the invention is useful for preventing, treating
CC and diagnosing neurological diseases or CNS disorders, such as:
CC Alzheimer's disease; Creutzfeldt-Jakob disease; Huntington's chorea; viral
CC infections of the brain; brain tumours; lysosomal storage diseases;
CC Parkinson's disease; and multiple sclerosis. The present amino acid
CC sequence represents a protein which was used in the invention
XX
XX Sequence 239 AA;
SQ
Query Match 79.2%; Score 1010.5; DB 6; Length 239;
Best Local Similarity 79.8%; Pred. No. 8.3e-60;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;
OY 2 QVOLOQSGPELEKPGASVYKLSCKASGYGFTGYTMVMVQSHKSLFWIGLITPPYNGASGY 61
DB 1 QVKLOESGAEIVRPVSVKISCKSGGYFTDVMHVMVQSHKSLFWIGLITPPYNGASGY 60
OY 62 NOKFPGKATLVYDKSSSTAYMDLSTSPDSAVYFCARG---GYDGRGPDYQGQSTTVTV 118
DB 61 NOKFPGKATLVYDKSSSTAYMDLSTSPDSAVYFCARGATMSY---FDYWGQVTVTV 116
OY 119 SSGVGSGSGGSGGSGGSDIELTQSPAIMSASPGKVTWTCSSASSVSYMWYQKSGTSP 178
DB 117 SSGGSGSGGSGGSGGSDIELTQSPAIMSASPGKVTWTCSSASSISYMWYQKSGTSP 176
OY 179 KRWIYDTSKLASGVGRPSGSGSGNSYSITLTSVEAEDDATYYCQOMSGYPLTFGAGTKL 238
DB 177 KRWIYDTSKLASGVGRPSGSGSGNSYSITLTSVEAEDDATYYCQOMSGYPLTFGAGTKL 236
OY 239 EIK 241
DB 237 EIK 239
XX
XX RESULT 7
XX ADJ88113
XX ID ADJ88113 standard; protein; 239 AA.
XX
XX AC ADJ88113;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human beta amyloid peptide antibody (508) heavy chain protein.
XX
XX Neurological disease; central nervous system; CNS disorder;
XX plaque-forming disease; Alzheimer's disease; SAA amyloidosis;
XX hereditary Icelandic syndrome; senility; multiple myeloma; scrapie;
XX bovine spongiform encephalopathy; BSE; kuru; Creutzfeldt-Jakob disease;
XX CJD; Gerstmann-Strausler-Sheinker disease; GSS; fatal familial insomnia;
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KW FFI; non-plaque-forming disease; Huntington's chorea; viral infection;
KW brain tumour; lysosomal storage disease; neurodegeneration;
KW multiple sclerosis; vaccine; beta amyloid peptide; beta AP; antibody;
KW human.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 31..35
XX /note="CDR1"
XX Region 50..66
XX /note="CDR2"
XX Region 99..107
XX /note="CDR3"
XX
XX US2004013647-A1.
XX
XX 22-JAN-2004.
XX
XX 11-MAR-2003; 2003US-00384788.
XX
XX 03-SEP-1999; 99US-0152417P.
XX 29-DEC-1999; 99US-00473653.
XX 31-JUL-2000; 2000US-00629971.
XX 31-AUG-2000; 2000WO-11000518.
XX 15-MAR-2001; 2001US-00808037.
XX 07-AUG-2001; 2001US-00830954.
XX 12-APR-2002; 2002US-0371735P.
XX 06-JUN-2002; 2002US-00162889.
XX
XX (UYRA-) UNIV RAMOT AT TEL AVIV LTD.
XX
XX Solomon B, Frenkel D;
XX
XX WPI, 2004-108188/11.
XX N-PSDB; ADJ88112.
XX
XX Treating neurological disease CNS e.g., Alzheimer's disease, by
PT displaying therapeutic molecule capable of treating the disease on viral
PT display vehicle which is then administered to subject through olfactory
PT system.
XX
XX Example 2; SEQ ID NO 6; 68pp; English.
XX
XX The invention relates to a method of treating a neurological disease or
CC disorder of the central nervous system (CNS). The method involves
CC displaying a therapeutic molecule capable of treating the neurological
CC disease or disorder of the CNS on a viral display vehicle and introducing
CC the viral display vehicle into a subject by applying an effective amount of
CC the viral display vehicle displaying the therapeutic molecule to an
CC olfactory system of the subject. The method is useful for treating a
CC neurological disease or disorder of CNS such as a plaque-forming disease
CC such as Alzheimer's disease, late onset Alzheimer's disease,
CC presymptomatic Alzheimer's disease, SAA amyloidosis, hereditary Icelandic
CC syndrome, senility, multiple myeloma, scrapie, bovine spongiform
CC encephalopathy (BSE), kuru, Creutzfeldt-Jakob disease (CJD), Gerstmann-
CC Strausler-Sheinker disease (GSS) or fatal familial insomnia (FFI). The
CC method is also useful for treating a non plaque forming disease or
CC disorder e.g. Huntington's chorea, viral infections of the brain, brain
CC tumours, lysosomal storage diseases which cause neurodegeneration and are
CC manifested by enzyme deficiencies and multiple sclerosis. The invention
CC is also used in the preparation of vaccines. The present sequence is
CC human beta amyloid peptide (beta AP) antibody heavy chain protein. This
CC sequence is used to illustrate the method of the invention.
XX
XX Sequence 239 AA;
SQ
Query Match 79.2%; Score 1010.5; DB 8; Length 239;
Best Local Similarity 79.8%; Pred. No. 8.3e-60;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;
OY 2 QVOLOQSGPELEKPGASVYKLSCKASGYGFTGYTMVMVQSHKSLFWIGLITPPYNGASGY 61
DB 1 QVKLOESGAEIVRPVSVKISCKSGGYFTDVMHVMVQSHKSLFWIGLITPPYNGASGY 60
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Db      1 QVKLGSGSELVPRGVSVKISCKSGYFTFDYAMHWKSHAKSLMIIGVISTYYGDASY 60
Qy      62 NQKFRGKATLVYDKSSSTAYMDLSTSEDSAVYFCARG---GYDRGFEDYMGQGTIVY 118
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 NQKFKGKATLVYDKSSSTAYMDLSTSEDSAVYFCARGTMY----FDYMGQGTIVY 116
Qy      119 SSGVGSGGGGGGGGSDIELTQSPAIMSASPEEKVTMTCSASSSVYMWYQOKSGTSP 178
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      117 SSGGGGGGGGGGGGSDIELTQSPAIMSASPEEKVTMTCSASSSVYMWYQOKSGTSP 176
Qy      179 KRWIVPTSLASGVPRFSGSGNSYSLTSSVEAEDDATYCCQWMSGYPLTFGAGTKL 238
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      177 KRWIVPTSLASGVPRFSGSGNSYSLTSSVEAEDDATYCCQWMSGYPLTFGAGTKL 236
Qy      239 EIK 241
        |||
Db      237 EIK 239

RESULT 8
ADT91213
ID      ADT91213 standard; protein; 261 AA.
AC      ADT91213;
DE      16-DEC-2004 (first entry)
XX      Single chain variable fragment (scfv) antibody #4.
XX      Tumour; benign intracranial meningioma; arteriovenous malformation;
XX      angioma; macular degeneration; melanoma; adenocarcinoma;
XX      malignant glioma; prostatic carcinoma; kidney carcinoma;
XX      bladder carcinoma; pancreatic carcinoma; thyroid carcinoma;
XX      lung carcinoma; colon carcinoma; rectal carcinoma; brain carcinoma;
XX      liver carcinoma; breast carcinoma; ovary carcinoma; angiofibroma;
XX      retrolental fibroplasia; haemangioma; Kaposi's sarcoma;
XX      single chain variable fragment; scfv; antibody.
XX      Unidentified.
XX      OS
XX      PN      US2004191249-A1.
XX      PD      30-SEP-2004.
XX      PF      20-OCT-2003; 2003US-00689006.
XX      PR      28-APR-2000; 2000WO-US011485.
XX      PR      09-NOV-2001; 2001US-00914605.
XX      PR      27-SEP-2002; 2002US-00259087.
XX      PA      (UYVA-) UNIV VANDERBILT.
XX      PI      Hallahan DE, Mernaugh R;
XX      DR      WPI; 2004-698661/68.
XX      DR      N-PSDB; ADT91212.
XX      PT      Screening phage-displayed antibodies binding to radiation-inducible
XX      PT      neointigen on cell, comprises contacting cell with antibodies, treating
XX      PT      cell with radiation, contacting cell with antibodies not binding to cell,
XX      PT      detecting bound antibody.
XX      PS      Claim 4; SEQ ID NO 24; 64pp; English.
XX      CC      The invention relates to a method for screening phage-displayed
XX      CC      antibodies binding to radiation-inducible neointigen on cell. The method
XX      CC      involves contacting cell with antibodies, treating cell with radiation,
XX      CC      contacting cell with antibodies not binding to cell and detecting the
XX      CC      bound antibody. The method is useful for screening several phage-
XX      CC      displayed antibodies for an ability to bind to a radiation-inducible
XX      CC      neointigen present on a cell, where the cell is tumour cell chosen from
XX      CC      benign intracranial meningiomas, arteriovenous malformation, angioma,
XX      CC      macular degeneration, melanoma, adenocarcinoma, malignant glioma,

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CC      prostatic carcinoma, kidney carcinoma, bladder carcinoma, pancreatic
CC      carcinoma, thyroid carcinoma, lung carcinoma, colon carcinoma, rectal
CC      carcinoma, brain carcinoma, liver carcinoma, breast carcinoma, ovary
CC      carcinoma, solid tumors, solid tumour metastases, angiofibroma,
CC      retrolental fibroplasia, haemangiomas, Kaposi's sarcoma, head and neck
CC      carcinomas and their combinations or vascular endothelial cell. The
CC      present sequence is a single chain variable fragment (scfv) antibody that
CC      binds to radiation-inducible neointigens.
XX      SQ      Sequence 261 AA;
XX      Query Match      78.6%; Score 1003; DB 8; Length 261;
XX      Best Local Similarity      80.9%; Pred. No. 2.9e-59;
XX      Matches 195; Conservative 17; Mismatches 27; Indels 2; Gaps 2;
Qy      2 QVLOOOSGPPELEKPKASVYLSCKASGYSPGYTMWVWQSHGKSLMIIGVISTYYGASGY 61
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      3 QVKLGSGSELVPRGVSVKISCKSGYFTFDYAMHWKSHAKSLMIIGVISTYYGDASY 62
Qy      62 NQKFRGKATLVYDKSSSTAYMDLSTSEDSAVYFCAR-GGYDRGFEDYMGQGTIVYSS 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      63 NQKFKGKATLVYDKSSTAYMDLSTSEDSAVYFCARWDGYG-GFSYMGQGTIVYSS 121
Qy      121 GVGSGGGGGGGGGSDIELTQSPAIMSASPEEKVTMTCSASSSVYMWYQOKSGTSPR 180
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      122 GGGGGGGGGGGGGSDIELTQSPAIMSATLGEKVTMCSASSSVYMWYQOKSGASPKL 181
Qy      181 WIYDPTSLASGVPRFSGSGNSYSLTSSVEAEDDATYCCQWMSGYPLTFGAGTKLEI 240
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      182 WIYYSNLSASVPRFSGSGNSYSLTSSVEAEDDATYCCQWMSGYPLTFGAGTKLEI 241
Qy      241 K 241
        |
Db      242 K 242

RESULT 9
ADC79232
ID      ADC79232 standard; protein; 239 AA.
AC      ADC79232;
DE      01-JAN-2004 (first entry)
XX      Control scfv VK-8-4.5 amino acid sequence.
XX      DE
XX      KW      CA 125 tumour antigen; CA 125 tumour antigen modulator;
XX      KW      CA 125 tumour antigen-associated disease; cytostatic; gene therapy.
XX      OS      Synthetic.
XX      PN      WO2003076465-A2.
XX      PD      18-SEP-2003.
XX      PF      11-MAR-2003; 2003WO-CA000341.
XX      PR      11-MAR-2002; 2002US-0363306P.
XX      PR      28-FEB-2003; 2003CA-02420494.
XX      PA      (UYSH ) UNIV SHERBROOKE.
XX      PI      Rancourt C, Piche A, Beaudin J;
XX      DR      WPI; 2003-722323/68.
XX      PT      New modulator capable of negatively modulating a CA 125 tumor antigen in
XX      PT      a mammalian cell, useful for preparing a composition for preventing or
XX      PT      treating CA 125 tumor antigen-associated disease in a mammal.
XX      PS      Disclosure; Fig 29C; 90pp; English.
XX      CC      The present invention describes a modulator capable of negatively

```

CC modulating a CA 125 tumour antigen in a mammalian cell. Also described:
CC (1) a recombinant nucleic acid comprising at least one sequence selected
CC from the group consisting of ADC79233, ADC79234, ADC79235, ADC79236,
CC ADC79237 and ADC79238; (2) a vector comprising the recombinant nucleic
CC acid; (3) a host cell; (4) a pharmaceutical composition; (5) preventing
CC or treating CA 125 tumour antigen-associated disease in a mammal; and (6)
CC negatively modulating a CA 125 tumour antigen in a mammalian cell. A
CC modulator capable of negatively modulating a CA 125 tumour antigen has
CC cyrostatic activity and can be used in gene therapy. The modulator, as
CC recombinant nucleic acid, vector or host cell can be used for preparing a
CC composition for preventing or treating CA 125 tumour antigen-associated
CC disease in a mammal. The present sequence is used in the exemplification
CC of the present invention.

XX Sequence 239 AA:
SQ

Query Match 78.3%; Score 998.5; DB 7; Length 239;
Best Local Similarity 79.4%; Pred. No. 5.3e-59;
Matches 193; Conservative 14; Mismatches 29; Indels 7; Gaps 2;

QY 2 QVQLQSGPELEKRGASVKLSCKASGYFTGYTMNWVQSHGKSLIEWIGLITPNYGASGY 61
Db 1 QVQLQSGPELVKPKASVYKISKASGYFTDYNMHWQSHGKSLIEWIGIYIPYNGDTGY 60

QY 62 NQKFRKATLVVDKSSSTAYMDLSTLTSBDSAVYFCARGG---YDGRGFDYWGQGTITV 118
Db 61 NQKFRNKASLTVDTSSTAYMELNLSLTSBDSAVYVMASSGGFWY---FDWVGQGTITV 116

QY 119 SSGVGGSGGGSGGGSDIELTQSPAIMSASPGKVTMTCSASSSVSYMHWYQOKSGTSP 178
Db 117 SSGGGSGGGSGGGSDIQMTQSPAILLSASPGKVTMTCRATPVSVMHWYQOKPGSSP 176

QY 179 KRMIYDTSKLASGVPRSGSGSGNSYSLTSSVFAEDDAIYYCOQMSGYLTGAGTKL 238
Db 177 KPMIYTTSNLASGVPARFSGSGSGTSYSLTVSRVEADDAIYYCOQMSRSPPTFGAGKL 236

QY 239 EIK 241
Db 237 EIK 239

RESULT 10
ADC79231
ID ADC79231 standard; protein; 239 AA.
XX
AC ADC79231;
XX
DT 01-JAN-2004 (first entry)
XX
DE Anti-CA125 scFvs VK-8-1.9 amino acid sequence.
XX
KW CA 125 tumour antigen; CA 125 tumour antigen modulator;
KW CA 125 tumour antigen-associated disease; cyrostatic; gene therapy.
XX
OS Synthetic.
XX
PN WO2003076465-A2.
XX
PD 18-SEP-2003.
XX
PE 11-MAR-2003; 2003WO-CA000341.
XX
PR 11-MAR-2002; 2002US-0363306P.
PR 28-FEB-2003; 2003CA-02420494.
XX
PA (UYSH) UNIV SHERBROOKE.
XX
PI Rancourt C, Piche A, Beaudin J;
XX
DR WPI; 2003-722323/68.
XX
PT New modulator capable of negatively modulating a CA 125 tumor antigen in
PT a mammalian cell, useful for preparing a composition for preventing or

PT treating CA 125 tumor antigen-associated disease in a mammal.
XX
XX Disclosure; Fig 29C; 90pp; English.
XX
XX The present invention describes a modulator capable of negatively
CC modulating a CA 125 tumour antigen in a mammalian cell. Also described:
CC (1) a recombinant nucleic acid comprising at least one sequence selected
CC from the group consisting of ADC79233, ADC79234, ADC79235, ADC79236,
CC ADC79237 and ADC79238; (2) a vector comprising the recombinant nucleic
CC acid; (3) a host cell; (4) a pharmaceutical composition; (5) preventing
CC or treating CA 125 tumour antigen-associated disease in a mammal; and (6)
CC negatively modulating a CA 125 tumour antigen in a mammalian cell. A
CC modulator capable of negatively modulating a CA 125 tumour antigen has
CC cyrostatic activity and can be used in gene therapy. The modulator, as
CC recombinant nucleic acid, vector or host cell can be used for preparing a
CC composition for preventing or treating CA 125 tumour antigen-associated
CC disease in a mammal. The present sequence is used in the exemplification
CC of the present invention.

XX Sequence 239 AA:
SQ

Query Match 78.2%; Score 997.5; DB 7; Length 239;
Best Local Similarity 79.4%; Pred. No. 6.2e-59;
Matches 193; Conservative 14; Mismatches 29; Indels 7; Gaps 2;

QY 2 QVQLQSGPELEKRGASVKLSCKASGYFTGYTMNWVQSHGKSLIEWIGLITPNYGASGY 61
Db 1 QVQLQSGPELVKPKASVYKISKASGYFTDYNMHWQSHGKSLIEWIGIYIPYNGDTGY 60

QY 62 NQKFRKATLVVDKSSSTAYMDLSTLTSBDSAVYFCARGG---YDGRGFDYWGQGTITV 118
Db 61 NQKFRNKASLTVDTSSTAYMELNLSLTSBDSAVYVMASSGGFWY---FDWVGQGTITV 116

QY 119 SSGVGGSGGGSGGGSDIELTQSPAIMSASPGKVTMTCSASSSVSYMHWYQOKSGTSP 178
Db 117 SSGGGSGGGSGGGSDIQMTQSPAILLSASPGKVTMTCRATPVSVMHWYQOKPGSSP 176

QY 179 KRMIYDTSKLASGVPRSGSGSGNSYSLTSSVFAEDDAIYYCOQMSGYLTGAGTKL 238
Db 177 KPMIYTTSNLASGVPARFSGSGSGTSYSLTVSRVEADDAIYYCOQMSRSPPTFGAGTKL 236

QY 239 EIK 241
Db 237 EIK 239

RESULT 11
AAR79872
ID AAR79872 standard; protein; 242 AA.
XX
AC AAR79872;
XX
DT 02-JUL-1996 (first entry)
XX
DE Anti-EGFR single chain antibody (Clone 11 H 1).
XX
KW Single chain antibody; antibody; epidermal growth factor receptor; EGFR;
KW tumour; cancer; glioma; melanoma; carcinoma; diagnosis; assessment;
KW phage antibody library.
XX
OS Mus musculus.
XX
PN WO9525167-A1.
XX
PD 21-SEP-1995.
XX
PE 16-MAR-1995; 95WO-EP000978.
XX
PR 17-MAR-1994; 94EP-00104160.
PR 02-DEC-1994; 94EP-00118970.
XX
PA (MERCK) MERCK PATENT GMBH.
XX

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PI Kettleborough AC, Bendig MM, Ansell KH, Guessow D, Adan J;
PI Mitjans F, Rosell E, Blasco F, Pinlats J;
DR WPI: 1995-336972/43.
DR N-PSDB; AAT04025.
XX
XX Anti-EGFR antibodies and single chain Fv antibody fragments - obtained
PT from phage-antibody libraries, useful for diagnosis and therapy of
PT tumours.
XX
XX Claim 4; Page 72-73; 93pp; English.
XX
XX Anti-epidermal growth factor receptor (EGFR) single chain antibodies and
CC antibodies constructed from anti-EGFR antibody fragments can be used for
CC diagnosis of tumours and assessment of tumour growth in vitro and in
CC vivo. They may also be used in a pharmaceutical composition for the
CC therapy of e.g. melanomas, gliomas and carcinomas. The antibodies and
CC fragments are derived from mice but are humanised so as to cause minimum
CC reaction against them. They are produced using the phage antibody
CC library. They are produced using the phage antibody library. (See
CC AAT04011-T04026 and AAR79858-R79873)
CC
XX
SQ Sequence 242 AA;

Query Match 78.0%; Score 995; DB 2; Length 242;
Best Local Similarity 79.8%; Pred. No. 9.2e-59;
Matches 193; Conservative 17; Mismatches 30; Indels 2; Gaps 1;

QY 2 QVQLQSGPELEKPGASVYLSCKASGYSTGYTMNWVKQSHKSLWIGLITPYNGASSY 61
DB 1 EVQLQSGAEIVKPGASVYLSCKASGYTFTSHMHMWKQAGGLEWISFNSNGRTNY 60
QY 62 NQKFRKATLTVDKSSSTAYMDLLSTSEDSAVYFCARG--GYDGRFDYWGQGITVTVS 119
DB 61 NEKFKSKATLTVDKSSSTAYMQLSLTSEDSAVYFCASRDYDGRFDYWGQGITVTVS 120
QY 120 SGVGGSGGGGGGGGGGSDIELTQSPAIMSASPGKVTMTCSASSSVSYMHVYQOKSGTSPK 179
DB 121 SGGGSGGGGGGGGGGSDIELTQSPSISMSASPGKVTMTCSASSSVSYMYWYQOKTSSPR 180
QY 180 RMYIDTSKLASGYVPGFSGSGSGNSYSLTISVYEADDDATYYCOQMSGYPLTFGAGTKLE 239
DB 181 LLTYDTSNLASGYVPRFSGSGSGTSLTISRMEADDAITYYCOQMSYPTHTGAGTKLE 240
QY 240 IK 241
DB 241 IK 242

RESULT 12
AAR79867
ID AAR79867 standard; protein; 244 AA.
XX
XX AAR79867;
AC
XX
XX 02-UTL-1996 (first entry)
DT
XX
XX Anti-EGFR single chain antibody (Clone 10 D 2).
DE
XX
XX Single chain antibody; antibody; epidermal growth factor receptor; EGFR;
KM tumour; cancer; glioma; melanoma; carcinoma; diagnosis; assessment;
KW phage antibody library.
XX
XX Mus musculus.
XX
XX W09525167-A1.
PN
XX
XX 21-SEP-1995.
PD
XX
XX 16-MAR-1995; 95MO-EP000978.
PF
XX
XX 17-MAR-1994; 94EP-00104160.
PR 02-DEC-1994; 94EP-00118970.
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XX
XX (MERCK ) MERCK PATENT GMBH.
PA
XX Kettleborough AC, Bendig MM, Ansell KH, Guessow D, Adan J;
XX PI Mitjans F, Rosell E, Blasco F, Pinlats J;
PI
XX WPI: 1995-336972/43.
DR
DR N-PSDB; AAT04020.
XX
XX Anti-EGFR antibodies and single chain Fv antibody fragments - obtained
PT from phage-antibody libraries, useful for diagnosis and therapy of
PT tumours.
XX
XX Claim 4; Page 60-61; 93pp; English.
XX
XX Anti-epidermal growth factor receptor (EGFR) single chain antibodies and
CC antibodies constructed from anti-EGFR antibody fragments can be used for
CC diagnosis of tumours and assessment of tumour growth in vitro and in
CC vivo. They may also be used in a pharmaceutical composition for the
CC therapy of e.g. melanomas, gliomas and carcinomas. The antibodies and
CC fragments are derived from mice but are humanised so as to cause minimum
CC reaction against them. They are produced using the phage antibody
CC library. They are produced using the phage antibody library. (See
CC AAT04011-T04026 and AAR79858-R79873)
CC
XX
SQ Sequence 244 AA;

Query Match 77.8%; Score 993; DB 2; Length 244;
Best Local Similarity 79.9%; Pred. No. 1.3e-58;
Matches 195; Conservative 14; Mismatches 31; Indels 4; Gaps 2;

QY 2 QVQLQSGPELEKPGASVYLSCKASGYSTGYTMNWVKQSHKSLWIGLITPYNGASSY 61
DB 1 EVQLQSGAEIVKPGASVYLSCKASGYTFTSHMHMWKQAGGLEWISFNSNGRTNY 60
QY 62 NQKFRKATLTVDKSSSTAYMDLLSTSEDSAVYFCARG--GYDGRFDYWGQGITVTVS 119
DB 61 NEKFKSKATLTVDKSSSTAYMQLSLTSEDSAVYFCASRDYDGRFDYWGQGITVTVS 120
QY 120 SGVGGSGGGGGGGGGGSDIELTQSPAIMSASPGKVTMTCSASSSVSYMHVYQOKSGTSPK 179
DB 121 SGGGSGGGGGGGGGGSDIELTQSPSISMSASPGKVTMTCSASSSVSYMYWYQOKPGSSPR 180
QY 180 RMYIDTSKLASGYVPGFSGSGSGNSYSLTISVYEADDDATYYCOQMSGYPLTFGAGTK 237
DB 181 LLTYDTSNLASGYVPRFSGSGSGTSLTISRMEADDAITYYCOQMSYPTHTGAGTK 240
QY 238 LEIK 241
DB 241 LEIK 244

RESULT 13
ABR62131
ID ABR62131 standard; protein; 242 AA.
XX
XX ABR62131;
AC
XX
XX 29-AUG-2003 (first entry)
DT
XX
XX Single chain antibody amino acid sequence #SRQ ID 18.
DE
XX
XX Tumour; drug delivery; ligand; cancer; carcinoma; bladder; breast;
KW cervix; colorectum; lung; ovary; pancreas; prostate; stomach;
KM cholangiocarcinoma; gastric sarcoma; glioma; lymphoma; melanoma;
KW multiple myeloma; osteosarcoma; head; neck; radiation; antibody.
XX
XX Synthetic.
XX
XX W02003028640-A2.
PN
XX
XX 10-APR-2003.
PD
```


PF 27-SEP-2002; 2002WO-US030917.
XX
XX 03-OCT-2001; 2001US-0328123P.
XX
XX (UYVA-) UNIV VANDERBILT.
XX
XX Hallahan DE, Qu S;
XX
XX WPI, 2003-421186/39.
XX
XX N-PSDB; ACC83314.
PT Identifying molecule that binds to irradiated tumor in a subject, by
PT exposing tumor to ionizing radiation, administering library of diverse
PT molecules and isolating library molecules from tumor to identify the
PT target.
XX
XX Claim 38; Page 105-106; 108pp; English.
XX
XX The invention relates to a method for identifying a molecule that binds
CC an irradiated tumor in a subject. The method of the invention involves
CC exposing a tumor to ionizing radiation, administering a library of
CC diverse molecules to a subject, and isolating one or more molecules of
CC the library from the tumor. The method of the invention is useful for
CC identifying a molecule that binds an irradiated tumor in a subject e.g.
CC warm-blooded vertebrate and human, and also for tumor detection. The
CC tumor is a primary or a metastasized tumor such as carcinoma of the
CC bladder, breast, cervix, colorectum, lung, ovary, pancreas, prostate,
CC stomach, cholangiocarcinoma, gastric sarcoma, glioma, lymphoma, melanoma,
CC multiple myeloma, osteosarcoma, head and neck tumor and solid tumor. The
CC method of the invention is useful for X-ray-guided delivery of a
CC therapeutic composition, a diagnostic composition or their combinations
CC to a tumor in a subject. The current sequence represents a single chain
CC antibody sequence that was identified following in vivo panning to
CC irradiated tumours. This antibody binds P-selectin
XX
SQ Sequence 242 AA;
Query Match 77.5%; Score 989.5; DB 6; Length 242;
Best Local Similarity 80.4%; Pred. No. 2.1e-58;
Matches 193; Conservative 14; Mismatches 32; Indels 1; Gaps 1;
QY 2 QVQLQQSGPELEKPKASVYKLSCKAGSYFTGYTMVMVQSHGKSLIEWIGLITPPYNGASSY 61
DB 3 QVQLQQSGAEIWMFPAASVYKMSCKAGYFTFTYMMWVQKRPQGLBWLGAIDTSDSYSY 62
QY 62 NQKFRGKATLTVDKSSSTAYMDLSTLSEDAVYFCARGYDGRFDYWGQGTITVSSG 121
DB 63 NQKFRGKATLTVDESSSTAYWQLSLTSEDAVYVCARGYYS-AFDYWGQGTITVSSG 121
QY 122 VGGSGGGSGGGSDIELTQSPAIMSASPGKVTMTCSASSSVSYMHYQOKSGTSPRW 181
DB 122 GGGSGGGSGGGSDIELTQSPPTMAASPGKVTITCRASSSVSYMHWFQOKSGTSPRW 181
QY 182 IYDTSKLASGVPRSGSGSGNSYSLTSSVEAEDATYTCQMGYPLTFAGTKLEIK 241
DB 182 IYDTSKLASGVPRSGSGSGTSTSLTSSMEADDAITYCLQKSSYPTFGAGTKLEIK 241
RESULT 14
ADT91207
ID ADT91207 standard; protein; 242 AA.
XX
XX ADT91207;
XX
XX 16-DEC-2004 (first entry)
XX
XX Single chain variable fragment (scFv) antibody #1.
XX
XX Tumour; benign intracranial meningioma; arteriovenous malformation;
XX anglioma; macular degeneration; melanoma; adenocarcinoma;
XX malignant glioma; prostatic carcinoma; kidney carcinoma;
XX bladder carcinoma; pancreatic carcinoma; thyroid carcinoma;
XX lung carcinoma; colon carcinoma; rectal carcinoma; brain carcinoma;

KW liver carcinoma; breast carcinoma; ovary carcinoma; angliofibroma;
KW retrorenal fibroplasia; haemangioma; Kaposi's sarcoma;
KW single chain variable fragment; scFv; antibody.
XX
XX unidentified.
XX
XX US2004191249-A1.
XX
XX
XX 30-SEP-2004.
XX
XX
XX 20-OCT-2003; 2003US-00689006.
XX
XX
XX 28-APR-2000; 2000WO-US011485.
XX
XX 09-NOV-2001; 2001US-00914605.
XX
XX 27-SEP-2002; 2002US-00259087.
XX
XX (UYVA-) UNIV VANDERBILT.
XX
XX Hallahan DE, Mernaugh R;
XX
XX WPI, 2004-698661/68.
XX
XX N-PSDB; ADT91206.
PT Screening phage-displayed antibodies binding to radiation-inducible
PT neointigen on cell, comprises contacting cell with antibodies, treating
PT cell with radiation, contacting cell with antibodies not binding to cell,
PT detecting bound antibody.
XX
XX Claim 4; SEQ ID NO 18; 64pp; English.
XX
XX The invention relates to a method for screening phage-displayed
CC antibodies binding to radiation-inducible neointigen on cell. The method
CC involves contacting cell with antibodies, treating cell with radiation,
CC contacting cell with antibodies not binding to cell and detecting the
CC bound antibody. The method is useful for screening several phage-
CC displayed antibodies for an ability to bind to a radiation-inducible
CC neointigen present on a cell, where the cell is tumour cell chosen from
CC benign intracranial meningiomas, arteriovenous malformation, anglioma,
CC macular degeneration, melanoma, adenocarcinoma, malignant glioma,
CC prostatic carcinoma, kidney carcinoma, bladder carcinoma, pancreatic
CC carcinoma, thyroid carcinoma, lung carcinoma, colon carcinoma, rectal
CC carcinoma, brain carcinoma, liver carcinoma, breast carcinoma, ovary
CC carcinoma, solid tumours, solid tumour metastases, angiofibromas,
CC retrolental fibroplasia, haemangiomas, Kaposi's sarcoma, head and neck
CC carcinomas and their combinations or vascular endothelial cell. The
CC present sequence is a single chain variable fragment (scFv) antibody that
CC binds to radiation-inducible neointigene.
XX
SQ Sequence 242 AA;
Query Match 77.5%; Score 989.5; DB 8; Length 242;
Best Local Similarity 80.4%; Pred. No. 2.1e-58;
Matches 193; Conservative 14; Mismatches 32; Indels 1; Gaps 1;
QY 2 QVQLQQSGPELEKPKASVYKLSCKAGSYFTGYTMVMVQSHGKSLIEWIGLITPPYNGASSY 61
DB 3 QVQLQQSGAEIWMFPAASVYKMSCKAGYFTFTYMMWVQKRPQGLBWLGAIDTSDSYSY 62
QY 62 NQKFRGKATLTVDKSSSTAYMDLSTLSEDAVYFCARGYDGRFDYWGQGTITVSSG 121
DB 63 NQKFRGKATLTVDESSSTAYWQLSLTSEDAVYVCARGYYS-AFDYWGQGTITVSSG 121
QY 122 VGGSGGGSGGGSDIELTQSPAIMSASPGKVTMTCSASSSVSYMHYQOKSGTSPRW 181
DB 122 GGGSGGGSGGGSDIELTQSPPTMAASPGKVTITCRASSSVSYMHWFQOKSGTSPRW 181
QY 182 IYDTSKLASGVPRSGSGSGNSYSLTSSVEAEDATYTCQMGYPLTFAGTKLEIK 241
DB 182 IYDTSKLASGVPRSGSGSGTSTSLTSSMEADDAITYCLQKSSYPTFGAGTKLEIK 241
RESULT 15
AAR79870

Search completed: October 24, 2005, 20:02:54
JOD time : 173 secs

```
ID AAR79870 standard; protein; 242 AA.
XX
XX AAR79870;
AC
XX
XX 02-JUL-1996 (first entry)
DT
XX
XX .Anti-EGFR single chain antibody (Clone 5 F 1).
DE
XX
XX Single chain antibody; antibody; epidermal growth factor receptor; EGFR;
KW tumour; cancer; glioma; melanoma; carcinoma; diagnosis; assessment;
XX phage antibody library.
XX
OS Mus musculus.
XX
XX WO9525167-A1.
XX
XX 21-SEP-1995.
XX
XX 16-MAR-1995; 95WO-EP000978.
XX
XX 17-MAR-1994; 94EP-00104160.
XX
XX 02-DEC-1994; 94EP-00118970.
XX
XX (MERE ) MERCK PATENT GMBH.
XX
XX Kettleborough AC, Bendig MM, Ansell KH, Gnessow D, Adan J;
XX Miltjans F, Rosell E, Blasco F, Piuats J;
XX
XX WPI; 1995-336972/43.
XX
XX N-PSDB; AAT04023.
XX
XX Anti-EGFR antibodies and single chain Fv antibody fragments - obtained
XX from phage-antibody libraries, useful for diagnosis and therapy of
XX tumours.
XX
XX
XX Claim 4; Page 67-68; 93pp; English.
XX
XX Anti-epidermal growth factor receptor (EGFR) single chain antibodies and
XX antibodies constructed from anti-EGFR antibody fragments can be used for
XX diagnosis of tumours and assessment of tumour growth in vitro and in
XX vivo. They may also be used in a pharmaceutical composition for the
XX therapy of e.g. melanomas, gliomas and carcinomas. The antibodies and
XX fragments are derived from mice but are humanised so as to cause minimum
XX reaction against them. They are produced using the phage antibody
XX library. They are produced using the phage antibody library. (See
XX AAT04011-T04026 and AAR79858-R79873)
XX
XX
XX Sequence 242 AA:
SQ
Query Match 77.4%; Score 987; DB 2; Length 242;
Best Local Similarity 79.3%; Pred. No. 3.1e-58;
Matches 192; Conservative 16; Mismatches 32; Indels 2; Gaps 1;
QY 2 QVQLQSGPELEKPGASVKLSCKRSGYSFTGYTMNWTKQSHGKSLIEWIGLITPYNGASSY 61
DB 1 QVRLQSGAEIVKRGASVKLSCKRSGYFTFSHMHWKQRAQGLIEWIGLITPYNGASSY 60
QY 62 NQKFRGKATLVDSSTAYMDLILTSBDAVYFCARG--GYDGRGFDYWGQGTIVTVS 119
DB 61 NEKFKSKATLVDSSTAYMDLILTSBDAVYFCARG--GYDGRGFDYWGQGTIVTVS 120
QY 120 SGVGGSGGGSGGGSDIELTQSPAIMSAPGEKVTMTCSASSSVSYMHWYQOKSGTSFK 179
DB 121 SGGSGSGGGSGGGSDIELTQSPAIMSAPGEKVTMTCSASSSVSYMHWYQOKSGTSFK 180
QY 180 RMIYDTSKLASGVGRFGSGSGSYSLTISVVEADATYYCOOWSGYPLTFGAGTKLE 239
DB 181 LLIVDTSNLASGVGRFGSGSGSYSLTISVVEADATYYCOOWSGYPLTFGAGTKLE 240
QY 240 IK 241
DB 241 IK 242
```

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OM protein - protein search, using sw model

Run on: October 24, 2005, 18:45:55 ; Search time 40 Seconds
(without alignments)
579.706 Million cell updates/sec

Title: US-09-979-539-1

Perfect score: 1276

Sequence: 1 MQVQLQSGPELEKPKGASVK.....CQWNGVPLTFGATKLEIK 241

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	850.5	66.7	268	2 A56446	Ig heavy chain V r
2	733	57.4	249	2 S41374	single chain Fv an
3	663	52.0	233	2 JC5322	p53 specific singl
4	529	41.5	144	2 B30502	Ig heavy chain V r
5	516.5	40.5	122	2 PH0887	Ig heavy chain V r
6	513.5	40.2	137	2 H32513	Ig heavy chain pre
7	503.5	39.5	120	2 E45722	anti-glycoprotein
8	502	39.3	130	1 JL0079	Ig kappa chain pre
9	501.5	39.3	119	2 F30502	Ig kappa chain V r
10	501	39.3	119	2 PH0099	Ig heavy chain V r
11	500.5	39.2	114	2 S25319	Ig heavy chain V r
12	499	39.1	103	2 S25591	Ig kappa chain V r
13	499	39.1	107	2 A30562	Ig kappa chain V r
14	496.5	38.9	120	2 F45722	anti-glycoprotein
15	496	38.9	107	2 B30562	Ig kappa chain V r
16	496	38.9	107	2 PC4405	Ig kappa chain V r
17	495.5	38.8	135	2 PS0057	Ig heavy chain pre
18	495	38.8	104	2 B45049	Ig kappa chain V r
19	495	38.8	106	2 PS0071	Ig kappa chain V r
20	495	38.8	235	2 S25058	Ig kappa chain - m
21	493.5	38.7	128	2 I37267	Ig heavy chain V r
22	492.5	38.6	118	1 MHMS38	Ig heavy chain V r
23	491.5	38.5	128	2 C37267	Ig heavy chain V r
24	487	38.2	119	2 B53285	Ig heavy chain V a
25	487	38.2	125	2 PH0100	Ig heavy chain V r
26	482.5	37.8	139	2 A27609	Ig heavy chain pre
27	482	37.8	107	2 S11119	Ig kappa chain V r
28	482	37.8	107	2 PT0398	Ig light chain V r
29	481.5	37.7	112	2 S09957	Ig heavy chain V-D

30	481	37.7	107	2 S11118	Ig kappa chain V r
31	478	37.5	107	2 PR0402	Ig light chain V r
32	478	37.5	107	2 S11121	Ig kappa chain V r
33	478	37.5	117	1 MHMS4E	Ig heavy chain V r
34	478	37.5	117	1 MHMSJ5	Ig heavy chain V r
35	478	37.5	140	2 T01407	Ig heavy chain (my
36	475	37.2	106	2 G27887	Ig kappa chain V r
37	474	37.1	107	2 PD0011	Ig kappa chain V r
38	474	37.1	120	2 A34871	Ig kappa chain V r
39	473.5	37.1	108	2 G30560	Ig kappa chain V r
40	473	37.1	107	2 PT0406	Ig kappa chain V r
41	472.5	37.0	120	2 A49982	Ig heavy chain V r
42	472.5	37.0	128	2 A37267	Ig heavy chain V r
43	472	37.0	107	2 PR0403	Ig light chain V r
44	471	36.9	118	2 PL0200	anti-DNA autoantib
45	470	36.8	100	2 S29590	Ig kappa chain V r

ALIGNMENTS

RESULT 1

A56446 Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C:Species: Mus musculus (house mouse)

C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996

C:Accession: A56446

R:Yang, F.W.; Folz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A:Title: A high affinity dispholxin-binding protein displayed on M13 is functionally identical to the dispholxin-binding protein of the dispholxin-producing bacteriophage

A:Reference number: A56446; MUID:95229583; PMID:7713873

A:Accession: A56446

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-268 <TRAN>

A:Cross-references: GB:U20617

C:Keywords: heterotrimer; immunoglobulin

Query Match

Best Local Similarity 66.7%; Score 850.5; DB 2; Length 268;

Matches 167; Conservative 25; Mismatches 47; Indels 1; Gaps 1;

QY	2	OVQLQSGPELEKPKGASVKYFTGYTMWVQSHQKSLFWIGLTPYNGASSY	61
DB	3	OVQLQSGPELEKPKGASVKYFTGYTMWVQSHQKSLFWIGLTPYNGASSY	62
QY	62	NQKFRKATLTVDKSSSTAYMDLSTSEDAVYFCARAGYDGRGPDYWGQTTVTS6G	121
DB	63	DPKFGKATLTVDKSSSTAYMDLSTSEDAVYFCARAGYDGRGPDYWGQTTVTS6G	121
QY	122	VGSGGGGSGGGGSDIELTQSPAIMSASPGKVTWTCGASSSVSYMHYIQKSGTSPKRW	181
DB	122	VGSGGGGSGGGGSDIELTQSPAIMSASPGKVTWTCGASSSVSYMHYIQKSGTSPKRW	181
QY	182	IYDTSKLASGVGRFSGSGGNSVSLTSSVBAEDATYTCQWNGVPLTFGATKLEIK	241
DB	182	IYDTSKLASGVGRFSGSGGNSVSLTSSVBAEDATYTCQWNGVPLTFGATKLEIK	241

RESULT 2

S41374 single chain Fv antibody - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C:Accession: S41374

R:Artaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.

A:Description: Construction and functional characterization of a single chain Fv antibody

A:Reference number: S41374

A:Accession: S41374

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-249 <ART>

A:Residues: 1-137 <KOF>
A:Cross-references: GB:M20831; NID:G196949; PIDN:AAA38848.1; PID:G196950
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 40.2%; Score 513.5; DB 2; Length 137;
Best Local Similarity 82.4%; Pred. No. 1.8e-27;
Matches 98; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 2 QVQLQSGPELEKPKASVYKLSCKASGYFTGYTMNWKSHGKSLIEWIGLITPYNGASSY 61
DB 20 EIQLOQSGAEIVKPKASVYKLSCKASGYFTGYTMNWKSHGKSLIEWIGLITPYNGASTSY 79
QY 62 NQKFRGKATLTVDKSSSTAYMDLSTLTSBDSAVYFCARGYDGRGPDYWGQGTITVVS 120
DB 80 NQKFRGKATLTVDKSSSTAYMDLSTLTSBDSAVYFCARKNY-GSPFDYWGQGTITVVS 137

RESULT 7

E45722
anti-glycoprotein H monoclonal antibody heavy-chain variable domain (Mab 5) - mouse (Ira
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: E45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdaloovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vaegu
J.; Vitol, 67; 499-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
A:Reference number: A45722; MUID:93100833; PMID:7677958
A:Accession: E45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-120 <SIM>
A>Note: sequence extracted from NCBI backbone (NCBI:P120593)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:15-99/Domain: immunoglobulin homology <IMM>

Query Match 39.5%; Score 503.5; DB 2; Length 120;
Best Local Similarity 79.2%; Pred. No. 7.3e-27;
Matches 95; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

QY 2 QVQLQSGPELEKPKASVYKLSCKASGYFTGYTMNWKSHGKSLIEWIGLITPYNGASS 60
DB 1 EIQLOQSGPELVKPKASVYKLSCKASGYFTGYTMNWKSHGKSLIEWIGLITPYNGASTS 60
QY 61 YNOKFRGKATLTVDKSSSTAYMDLSTLTSBDSAVYFCARGYDGRGPDYWGQGTITVVS 120
DB 61 YNOKFRGKATLTVDKSSSTAYMDLSTLTSBDSAVYFCARGYDGRGPDYWGQGTITVVS 120

RESULT 8

J10079

Ig kappa chain precursor V region (anti-phenylloxazalone 6F6) - mouse

C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999

C:Accession: J10079; A49044; B49044

R:Kaartinen, M.; Rocca-Serra, J.; Maekela, O.
Mol. Immunol. 25, 859-865, 1988

A:Title: Combinatorial association of V genes: one VH gene codes for three non-cross-re
A:Reference number: J10079; MUID:89096973; PMID:3211160

A:Accession: J10079
A:Molecule type: mRNA
A:Residues: 1-130 <KAA>
A:Cross-references: GB:M27792; NID:G197159
A:Experimental source: mRNA clones for anti-phenylloxazalone antibody 6F6
A>Note: the authors translated the codon TGC for residue 8 as Pro and TTC for residue 10
R:Milstein, C.; Even, U.; Jarvis, U.M.; Gonzalez-Fernandez, A.; Gherardi, E.
Eur. J. Immunol. 22, 1627-1634, 1992

A:Title: Non-random features of the repertoire expressed by the members of one V kappa g
A:Reference number: A49044; MUID:92289826; PMID:1601044

A:Accession: A49044

A:Molecule type: DNA
A:Residues: 1-25 <ML>
A:Cross-references: GB:S37663; NID:G250214; PIDN:AA822331.1; PID:G250217
A>Note: sequence extracted from NCBI backbone (NCBIN:106802, NCBI:P106809)
A:Accession: B49044
A:Molecule type: DNA
A:Residues: 114-116 <ML2>
A:Cross-references: GB:S37664; NID:G250215; PIDN:AA822332.1; PID:G250218
A:Experimental source: BALB/c germ-line
A>Note: sequence extracted from NCBI backbone (NCBIN:106807, NCBI:P106822)
C:Genetics:
A:Gene: V(kappa)Ox1
A:Intron: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kay
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1-
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-130/Product: Ig kappa chain V region (6F6) #status predicted <MAT>
F:38-111/Domain: immunoglobulin homology <IMM>
F:45-109/Disulfide bonds: #status predicted

Query Match 39.3%; Score 502; DB 1; Length 130;
Best Local Similarity 92.4%; Pred. No. 1e-26;
Matches 97; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 137 IEITSPAIMSAPSEKVTMTCSASSSVYMWYQKSGTSPKRWIYDTSKLASGVPGRF 196
DB 24 IYLTSPAIMSAPSEKVTMTCSASSSVYMWYQKSGTSPKRWIYDTSKLASGVPGRF 83
QY 197 SSGSGNSYSLTSSVEAEDDATYCCQWMSGYPLFRGAGTKLEIK 241
DB 84 SSGSGNSYSLTSSVEAEDDATYCCQWMSGYPLFRGAGTKLEIK 128

RESULT 9

F30502

Ig heavy chain V region (A52) - mouse

C:Species: Mus musculus (house mouse)
C:Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C:Accession: F30502

R:Elia, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988

A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mic
A:Reference number: A30502; MUID:88315787; PMID:2457627

A:Accession: F30502
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <EIL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 39.3%; Score 501.5; DB 2; Length 119;
Best Local Similarity 78.9%; Pred. No. 9.8e-27;
Matches 97; Conservative 9; Mismatches 8; Indels 9; Gaps 2;

QY 2 QVQLQSGPELEKPKASVYKLSCKASGYFTGYTMNWKSHGKSLIEWIGLITPYNGASSY 61
DB 1 EIQLOQSGAEIVKPKASVYKLSCKASGYFTGYTMNWKSHGKSLIEWIGLITPYNGASTSY 60
QY 62 NQKFRGKATLTVDKSSSTAYMDLSTLTSBDSAVYFC-----RGYDGRGPDYWGQGTITV 116
DB 61 NQKFRGKATLTVDKSSSTAYMDLSTLTSBDSAVYFCARGLRRGGY----FDYWGQGTITL 116

QY 117 TYS 119
DB 117 TYS 119

RESULT 10

P00099

Ig heavy chain V region (anti-cyclosporin F) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 21-Jan-2000

C/Accession: PH0099

R/Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quesniaux, V.F.J.; V

Mol. Immunol. 27, 1029-1038, 1990

A/Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.

A/Reference number: PH0087; MUID:91042649; PMID:2122240

A/Accession: PH0099

A/Molecule type: mRNA

A/Residues: 1-119 <SCH>

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

F/31-35/Region: complementarity-determining 1

F/50-66/Region: complementarity-determining 2

F/99-106/Region: complementarity-determining 3

Query Match 39.3%; Score 501; DB 2; Length 119;

Best Local Similarity 80.7%; Pred. No. 1.1e-26;

Matches 96; Conservative 11; Mismatches 10; Indels 2; Gaps 1;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSTGYTMNWYKSHGKSLWIGLITPYNGASSY 61

Db 1 EVQLQSGPELVHPGASMKISCKASGYSTGYTMWYKSHGKSLWIGLITPYNGSIAT 60

QY 62 NQFPGKATLVKSSSTAYMDLISLSEDAVYFCARGYDGRGPDYWGQGTITVYSS 120

Db 61 NQFPGKATLVKSSSTAYMDLISLSEDAVYFCARGY--YADYWGQGTITVYSS 117

RESULT 11

S26319

Ig heavy chain V region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 10-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000

C/Accession: S26319

R/Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A/Title: Antibodies that are specific for a single amino acid interchange in a protein e

A/Reference number: S26309; MUID:91341421; PMID:1908510

A/Accession: S26319

A/Molecule type: mRNA

A/Residues: 1-114 <STA>

A/Cross-references: EMBL:X59172

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/11-94/Domain: immunoglobulin homology <IMM>

Query Match 39.2%; Score 500.5; DB 2; Length 114;

Best Local Similarity 82.6%; Pred. No. 1.1e-26;

Matches 95; Conservative 8; Mismatches 11; Indels 1; Gaps 1;

QY 6 QQSGLPELEKPGASVKLSCKASGYSTGYTMNWYKSHGKSLWIGLITPYNGASSYNOKF 65

Db 1 QQSGLPELVKPGASVKISCKASGYSTGYTMNWYKSHGKSLWIGLITPYNGDTFVNOKF 60

QY 66 RGRATLVKSSSTAYMDLISLSEDAVYFCARGYDGRGPDYWGQGTITVYSS 120

Db 61 KGRATLVKSSSTAYMDLISLSEDAVYFCARGYDGRGPDYWGQGTITVYSS 114

RESULT 12

S29591

Ig kappa chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C/Accession: S29591

R/Kavaler, J.

submitted to the EMBL Data Library, April 1991

A/Reference number: S26459

A/Accession: S29591

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-103 <KAV>

A/Cross-references: EMBL:X59094; NID:952227; PIDN:CAA41820.1; PID:952228

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-88/Domain: immunoglobulin homology <IMM>

Query Match 39.1%; Score 499; DB 2; Length 103;

Best Local Similarity 93.2%; Pred. No. 1.2e-26;

Matches 96; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 137 IELTQSPAIMSAPGKVTMTCSASSSVSYMHYQOKSGTSPKRWIYDTSKLASGVPGRP 196

Db 1 IVLTSQPAIMSAPGKVTMTCSASSSVSYMHYQOKSGTSPKRWIYDTSKLASGVPAR 60

QY 197 SGGSGNSYSLTISVYAEADATYYCQOWSGYPLTFGAGTKLE 239

Db 61 SGGSGTYSYSLTISVYAEADATYYCQOWSNPLTFGAGTKLE 103

RESULT 13

A30562

Ig kappa chain V regions (27.7.2 and 27.4b.2) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000

C/Accession: A30562

R/Sikder, S.K.; Borden, P.; Guezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.

J. Immunol. 142, 888-893, 1989

A/Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bir

A/Reference number: A30562; MUID:89110066; PMID:2464031

A/Accession: A30562

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-107 <SIK>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/16-89/Domain: immunoglobulin homology <IMM>

Query Match 39.1%; Score 499; DB 2; Length 107;

Best Local Similarity 91.4%; Pred. No. 1.3e-26;

Matches 96; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 137 IELTQSPAIMSAPGKVTMTCSASSSVSYMHYQOKSGTSPKRWIYDTSKLASGVPGRP 196

Db 2 IVLTSQPAIMSAPGKVTMTCSASSSVSYMHYQOKSGTSPKRWIYDTSKLASGVPAR 61

QY 197 SGGSGNSYSLTISVYAEADATYYCQOWSGYPLTFGAGTKLEIK 241

Db 62 SGGSGTYSYSLTISVYAEADATYYCQOWSNPLTFGAGTKLEIK 106

RESULT 14

F45722

anti-glycoprotein H monoclonal antibody heavy-chain variable domain (Mab 33) - mouse (Irr

C/Species: Mus musculus (house mouse)

C/Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

C/Accession: F45722

R/Stimpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasque

J. Virol. 67, 489-496, 1993

A/Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hum

A/Reference number: A45722; MUID:93100833; PMID:7677958

A/Accession: F45722

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: nucleic acid

A/Residues: 1-120 <SIM>

A/Note: sequence extracted from NCBI backbone (NCBIRP.120594)

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: glycoprotein

F/15-99/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 38.9%; Score 496.5; DB 2; Length 120;

Matches 94; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

```

QY      2 OVQLQSGPELEKPGASVYLSCKASGYSTGYTMNWKSHGKSLIEWIGL-ITPYNGASS 60
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 EVQLQSGPELVKPGASVKISCKASGYSTGTITMNVKORHGKSLIEWIGLITPNNGGTS 60
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      61 YNOKFRGKATLTVDKSSSTAYMDLSTSEDSAVYFCARGGYDGRGFDYMGQGTITVTVSS 120
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 YNQRFRGKTTLTLDKSSSTVYVELLSTSEDSAVYFCARGFRDYALDSMGQGTISVTVS 120
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 15

```

B30562
Ig kappa chain V region (27.10.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C:Accession: B30562
R:Sticker, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.I.
J. Immunol. 142, 888-893, 1989
A:Title: Amino acid substitutions in V-H CDR2 change the idioctype but not the antigen-bi
A:Reference number: A30562; MUID:89110066; PMID:2464031
A:Accession: B30562
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <SIK>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-89/Domain: immunoglobulin homology <IMM>

```

```

Query Match      38.9%; Score 496; DB 2; Length 107;
Best Local Similarity 90.5%; Pred. No. 2e-26;
Matches 95; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

```

```

QY      137 IELTQSPAIMSASPEEKVTMTCSASSSVSMHWYQKSGTSPKRWIYDTSKLASGVPRF 196
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2 IVLTQSPAIMSASPEEKVTMTCSASSSVSMHWYQKSGTSPKRWYDTSKLASGVPTRF 61
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      197 SSGSGSGNSYSLTSSVEAEDDATYCCQWMSGYPLTFGAGTKLEIK 241
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      62 SSGSGSGTSLTSSMEADDAATYCCQWSSNPYTFGGGTKLEIK 106
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Search completed: October 24, 2005, 20:06:32
Job time : 41 secs

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OM protein - protein search, using sw model

Run on: October 24, 2005, 18:38:13 ; Search time 169 Seconds

(without alignments)
730.243 Million cell updates/sec

Title: US-09-979-539-1

Perfect score: 1276
Sequence: 1 MQVUQSGPBELEKRGASVK.....CQMSGYPTFGATKLEIK 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Key	Score	Query Match	Length	ID	Description
1	792.5	62.1	243	Q7QM2	Q7QM2 mus musculu
2	783.5	61.4	244	Q65ZC8	Q65ZC8 homo sapien
3	771.5	60.5	487	Q65ZL2	Q65ZL2 mus sp. tyv
4	733.5	57.5	255	Q6KB05	Q6KB05 mus musculu
5	726.5	56.9	241	Q921A6	Q921A6 mus musculu
6	720	56.4	298	Q9QYF0	Q9QYF0 synthetic c
7	718.5	56.3	240	Q65ZC9	Q65ZC9 homo sapien
8	645	50.5	248	Q65ZQ7	Q65ZQ7 mus sp. b3
9	628	49.2	218	Q925S1	Q925S1 mus musculu
10	543	42.6	170	Q925S2	Q925S2 mus musculu
11	514.5	40.3	470	Q7TMK1	Q7TMK1 mus musculu
12	502.5	39.4	472	Q6B7A7	Q6B7A7 mus musculu
13	496	38.9	112	Q8K1F0	Q8K1F0 mus musculu
14	495.5	38.8	488	Q91WR1	Q91WR1 mus musculu
15	492.5	38.6	118	HV51_MOUSE	HV51_MOUSE mus musculu
16	491	38.5	107	KV6F_MOUSE	KV6F_MOUSE mus musculu
17	486	38.1	107	KV6I_MOUSE	KV6I_MOUSE mus musculu
18	485	38.1	117	Q9QXE9	Q9QXE9 mus musculu
19	485	38.0	107	KV6H_MOUSE	KV6H_MOUSE mus musculu
20	485	38.0	120	Q920E8	Q920E8 mus musculu
21	484	37.9	107	KV6G_MOUSE	KV6G_MOUSE mus musculu
22	483	37.9	117	Q9QXF0	Q9QXF0 mus musculu
23	482	37.8	134	Q8VDD0	Q8VDD0 mus musculu
24	481.5	37.7	481	Q8VCV5	Q8VCV5 mus musculu
25	480	37.6	107	KV6J_MOUSE	KV6J_MOUSE mus musculu
26	478	37.5	117	HV13_MOUSE	HV13_MOUSE mus musculu
27	478	37.5	117	HV13_MOUSE	HV13_MOUSE mus musculu
28	473	37.1	134	Q65ZR6	Q65ZR6 mus musculu
29	472.5	37.0	112	Q9D8L4	Q9D8L4 mus musculu
30	468	36.7	112	Q8K1F2	Q8K1F2 mus musculu
31	467	36.6	465	Q6PJB2	Q6PJB2 mus musculu

32	466	36.5	123	2	Q8VJ1	Q8VJ1 mus musculu
33	462	36.2	136	1	HV15_MOUSE	HV15_MOUSE mus musculu
34	459	36.0	481	2	Q91WT1	Q91WT1 mus musculu
35	457	35.8	112	2	Q8K1F3	Q8K1F3 mus musculu
36	457	35.8	114	2	Q8K1F1	Q8K1F1 mus musculu
37	453.5	35.5	482	2	Q8K1F2	Q8K1F2 mus musculu
38	453	35.5	142	2	Q92401	Q92401 mus musculu
39	451	35.3	147	2	Q925S3	Q925S3 mus musculu
40	450.5	35.3	145	2	Q924R3	Q924R3 mus musculu
41	447.5	35.1	139	1	HV07_MOUSE	HV07_MOUSE mus musculu
42	447.5	35.1	145	2	Q924Q7	Q924Q7 mus musculu
43	447.5	35.1	145	2	Q924R1	Q924R1 mus musculu
44	445	34.9	120	1	HV03_MOUSE	HV03_MOUSE mus musculu
45	445	34.9	480	2	Q8K0Z4	Q8K0Z4 mus musculu

ALIGNMENTS

RESULT 1	ID	Q7QM2	PRELIMINARY;	PRT;	243 AA.
AC	Q7QM2				
DT	01-OCT-2003 (Tremblrel. 25, Created)				
DT	01-OCT-2003 (Tremblrel. 25, Last sequence update)				
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)				
DE	Scfv 6H8 protein (Fragment).				
GN	Name=scfv 6H8;				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-Balb/C;				
RX	MEDLINE=2285326; PubMed=12860977; DOI=10.1074/jbc.M306877200;				
RA	Peter J.C., Ettekhari P., Billiald P., Wallikar G., Hoebeke U.;				
RT	"scfv single chain antibody variable fragment as inverse agonist for				
RT	the beta-2 adrenergic receptor.";				
RL	J. Biol. Chem. 278:36740-36747(2003).				
DR	EMBL; AJ574851; CAB00495.1; -.				
DR	HSSP; P01751; 1A6W.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; Ig_v.				
DR	SMART; SM00406; IGV; 2.				
DR	PROSITE; PS50835; IG_LIKE; 2.				
FT	NON TER				
SQ	SEQUENCE 243 AA; 25976 MW; BEFF64D2DCFAF76 CRC64;				
Query Match	62.1%; Score 792.5; DB 2; Length 243;				
Best Local Similarity	64.9%; Pred. No. 4.1e-51;				
Matches	157; Conservative 30; Mismatches 48; Indels 7; Gaps 4;				
QY	2 QVUOQSGPELEKRPASVKLSCKASGYFTGYTMWVQSHKSLFWIGLITPNYGASSY 61				
DB	1 QVUOQSGSELYRPASVKLSCKASGYFTTYMWMVQRHQGLEWIGNIYPSGGINY 60				
QY	62 NQKFGKATLTFVDKSSFAVMDLISLTSEDSAVFECARGYDGRGFDYWGQSTTVTSVG 121				
DB	61 DEKFGKGLITVDTSSSTAVMHLISLASBDAVYICARG---GRGLDVGAGATTLTVSSG 117				
QY	122 VGGSGGGSGGGSDIELTQSPALMSAPGEKVTWTCASSSV-SYMFMYQKSGTSPKR 180				
DB	118 GGGSGGGSGGGSDIQWTQSSSSFSVSLGDRVITTCASEDIYRLAWYQKPNADRL 177				
QY	181 WYDTSKLSAGVPGFSGSGGNSYSLTSSVEADDTTYCCQ-WSGYPLTFGAGTKLE 239				
DB	178 LISGATSLFTGVPRFSGSGGKDYTLISLTQEDVATYYCCQYWS--TRTFGGTKLE 235				
QY	240 IK 241				
DB	236 IK 237				

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RESULT 2
Q65ZC8      PRELIMINARY;      PRT;      244 AA.
ID 065ZC8
AC 065ZC8
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97362799; PubMed=9219263;
RA Kontermann R.E., Wing M.G., Winter G.,
RT "Complete recruitment using bispecific diabodies.",
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13057; CAI73500.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PSS0835; IG_LIKE; 2.
FT NON_TER      1
FT 4NON_TER      1
FT SEQUENCE      244 AA; 26127 MW; 4B1F1786839F2BF CRC64;

Query Match      61.4%; Score 783.5; DB 2; Length 244;
Best Local Similarity 61.3%; Pred. No. 1.9e-50;
Matches 145; Conservative 39; Mismatches 52; Indels 3; Gaps 2;

QY      2 QVQLQSGPELEKPGASVKLSCKASGYSTFTGYTMNWVKQSHGKSLIEWIGLITPYNGASSY 61
DB      1 QVQLVQSGAEVKKPKQDSVKVSCKASGYTFSDHYMHWVROAPQGLEWMWIDPNNKGDTRF 60
QY      62 NQKFRGKATLTVDKSSSTAYMDLSTLSDSAVYFCARGYDGR--GFDVWGQGTITVVS 119
DB      61 AQRFGKATLTVRDTISIAAIVMEVSRLSDDTAIVVYCARBEGSAIYQMDVWGQGTITVVS 120
QY      120 SGVSGSGGGSGGSDIELTQSPAIMSASPGEKVTMTCSASSV--SYMHVYQOKSGTSP 178
DB      121 SGGSGSGGGSGGSDIQMTQSPSTLSASIGDVTITTCRASBGIYHMLANYQKPKKAP 180
QY      179 KRWIYDTSKLASGVPRFSGSGSGNSYSLTISVYAEADATYYCOQMSGYPLTFGAGTKL 238
DB      181 KFLIYKASLSLASGAPSRFSGSGSGTDPTLTITSSIQPDPFATYYCOQSNYPLTFGGGTKL 240
QY      239 EIK 241
DB      241 EIK 243

RESULT 3
Q65ZL2      PRELIMINARY;      PRT;      487 AA.
ID 065ZL2
AC 065ZL2
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE Single-chain Fv (Fragment).
GN Name=M4-IFN- $\epsilon$ tau;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96272580; PubMed=8688499;

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RA Qi Y., Xiang J.;
RT "A genetically engineered single-gene-encoded anti-TAG72 chimeric
RT antibody secreted from myeloma cells.";
RL Hum. Antibodies Hybridomas 6:161-166(1995).
DR EMBL; S82493; AAB37424.2; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-setc; 2.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00408; IGc2; 2.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_1.
DR SEQUENCE      487 AA; 53578 MW; C7BAB69F30555504 CRC64;

Query Match      60.5%; Score 771.5; DB 2; Length 487;
Best Local Similarity 63.5%; Pred. No. 3.2e-49;
Matches 133; Conservative 28; Mismatches 53; Indels 7; Gaps 3;

QY      2 QVQLQSGPELEKPGASVKLSCKASGYSTFTGYTMNWVKQSHGKSLIEWIGLITPYNGASSY 61
DB      20 QVQLQSGDAELVPGASVKISCKASGYTFTHAIHWAKKPKQGLEWIGIYISPGNDIKY 79
QY      62 NQKFRGKATLTVDKSSSTAYMDLSTLSDSAVYFCARGYDGRGVDYWGQGTITVVS 121
DB      80 NEKFRKATLTVDKSSSTAYMDLSTLSDSAVYFCRASY-----GHWGQGTITL-GSG 133
QY      122 VGSAGSGSGGGSDIELTQSPAIMSASPGEKVTMTCSASSV--SYMHVYQOKSGTSPR 180
DB      134 GGSAGSGSGGGSGSRQMTQSPASLSVSGELVITTCRASENIYSLNAYQKQKGSPL 193
QY      181 WIDYTSKLASGVPRFSGSGSGNSYSLTISVYAEADATYYCOQMSGYPLTFGAGTKLEI 240
DB      194 LVYAATNLADGVRSRFSGSGSGTGYSLKINSIQSDPFGSYQHFMTGYTFGGGTRLEI 253
QY      241 K 241
DB      254 K 254

RESULT 4
Q6KB05      PRELIMINARY;      PRT;      255 AA.
ID 06KB05
AC 06KB05
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Single-chain Fv (Fragment).
GN Name=scFv B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hoebeke J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ746180; CAG34081.1; -.
DR HSSP; P01837; 1KCR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PSS0835; IG_LIKE; 2.

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DT 25-OCT-2004 (TREMBlrel. 28, last sequence update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C1G/7;
RX MEDLINE=97362799; PubMed=9219263;
RA Kontemann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bioprecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL: Y13056; CAA73499.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00409; IG; 2.
DR SMART: SM00406; IGv; 2.
DR PROSITE: PSS0835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match 56.3%; Score 718.5; DB 2; Length 240;
Best Local Similarity 57.4%; Pred. No. 1.3e-45;
Matches 139; Conservative 43; Mismatches 55; Indels 5; Gaps 4;

QY 2 QVQLVQSGPELEKPGASVKLSCKASGYFTGYTMNWVKOSHGLEWIGLITPYNGASS- 60
DB 1 QVQLVQSGGGLVQPGSSLRISCAASGFTPSYGMHWVRQAPGKLEWVAIYS-YDGSNKY 59

QY 61 YNOKFRGKATLVYDKSSSTAYMDLISLTSEDAVYFCARGGYDGRGFDYWGQGTITVSS 120
DB 60 YADSVKGRFTISRDNKHTLYLQMNSTLRADETAVYCARPM--GDSLDPMKGTLLTVSS 117

QY 121 GVSGSGGGSGGGSDIELTQSPALMSAPGEKVTMCSASSV-SYMHVYQOKS 179
DB 118 GGGSGGGSGGGSDIQMTQSPFTLASIGDRVTTCRASEGILRWLAHYQOKPGAPK 177

QY 180 RWIYDTSKLASGVPRFSGSGNSYSLTISVAEDDATYCCQMGSGYPLTFGAGTKLE 239
DB 178 LLIYKASLASRAHSRFSGSGSDITLITSLQPDPAFYCCQYQYNYPLTFGAGTKLE 237

QY 240 IK 241
DB 238 IK 239

RESULT 8
Q65ZQ7 PRELIMINARY; PRT; 248 AA.
ID Q65ZQ7;
AC Q65ZQ7;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, last annotation update)
DE B3 (Fv)-PE40 (Fragment).
GN Name=B3 (Fv)-PE40;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92020904; PubMed=1924323;
RA Brinkmann U., Pai L.H., FitzGerald D.J., Willingham M., Pastan I.;
RT "B3 (Fv)-PE36DEL, a single-chain immunotoxin that causes complete
RT regression of a human carcinoma in mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
DR EMBL: S57990; AAB19971.2; -.

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DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00409; IG; 2.
DR SMART: SM00406; IGv; 2.
DR PROSITE: PSS0835; IG_LIKE; 2.
FT NON_TER 248
SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43B570950 CRC64;

Query Match 50.5%; Score 645; DB 2; Length 248;
Best Local Similarity 51.0%; Pred. No. 3.8e-40;
Matches 126; Conservative 41; Mismatches 74; Indels 6; Gaps 1;

QY 1 MOYVLQSGPELEKPGASVKLSCKASGYFTGYTMNWVKOSHGLEWIGLITPYNGASS 60
DB 1 MDYLVESGGGLVQPGSSLRISCAASGFTPSYGMHWVRQAPGKLEWVAIYSNDSSAA 60

QY 61 YNOKFRGKATLVYDKSSSTAYMDLISLTSEDAVYFCARGGYDGRGFDYWGQGTITVSS 120
DB 61 YSDTVKGRFTISRDNARNTLYLQMSRLKSEDPALYSCARGLAWGAFAYWGQGTLLTVSS 120

QY 121 GVSGSGGGSGGGSDIELTQSPALMSAPGEKVTMCSASSV-----SYMHVYQOKS 174
DB 121 GGGSGGGSGGGSDIVMTQSPSLPVSIGDQASISCRSSQITVHSNGNTLYEWLQRP 180

QY 175 GTSPEKRWIYDTSKLASGVPRFSGSGNSYSLTISVAEDDATYCCQMGSGYPLTFGA 234
DB 181 GQSPKLLIYKVSRRFSGVDRFSGSGSDITLITSLRVAEDLGYVYCFQGSIVPFTFS 240

QY 235 GTKLEIK 241
DB 241 GTKLEIK 247

RESULT 9
Q925S1 PRELIMINARY; PRT; 218 AA.
ID Q925S1;
AC Q925S1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE MRP5 (Fragment).
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C;
RC STRAIN=BALB/C;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL: AF240168; AAK43733.1; -.
DR HSSP: P01665; IQNZ.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PSS0835; IG_LIKE; 1.
FT NON_TER 218
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 49.2%; Score 628; DB 2; Length 218;
Best Local Similarity 55.8%; Pred. No. 6e-39;

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Matches 121; Conservative 35; Mismatches 55; Indels 6; Gaps 2;

QY 2 QVLOOOSPELEKPGASVYLSCASGYSFTGYTMNWKSHGKSLKLEWIGLITPPYGASGY 61
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QVKKLOOSPELEKPGASVYLSCASGYSFTGYTMNWKSHGKSLKLEWIGLITPPYGASGY 62
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 NOKFRGKATLTVDKSSSTAYMDLISLTSBDSAIVFCARGYDGR--GFDYWGQGTTVTVS 119
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 NOKFRGKATLTVDKSSSTAYMDLISLTSBDSAIVFCARGYDGR--GFDYWGQGTTVTVS 121
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 122 VGGSGGGGSGGGSDIELTQSPALMSASGEXEYMTCSASSV----SYMFWYQKSGT 176
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 122 GGGSGGGGSGGGSDIVLTQSPALMSASGEXEYMTCSASSV----SYMFWYQKSGT 181
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 177 SPKRWIYDTSKLASGVPGRFSGSGNSYSLTISSE 213
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 182 PKKLITVYASKQSGVPGAGLASSGSDTSPINITYPWE 218
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
Q925S2 PRELIMINARY; PRT; 170 AA.
AC Q925S2;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE MRPA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240167; AAK43732.1; -.
DR HSSP; P01751; IAGW.
DR SMART; SM00406; IGV, 1.
DR PROSITE; PS50835; IG_LIKE; 1.
SQ SEQUENCE 170 AA; 17978 MW; 5042823CC6C10F38 CRC64;

Query Match 42.6%; Score 543; DB 2; Length 170;
Best Local Similarity 66.4%; Pred. No. 9.4e-33;
Matches 101; Conservative 23; Mismatches 16; Indels 12; Gaps 2;

QY 2 QVLOOOSPELEKPGASVYLSCASGYSFTGYTMNWKSHGKSLKLEWIGLITPPYGASGY 61
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QVKKLOOSPELEKPGASVYLSCASGYSFTGYTMNWKSHGKSLKLEWIGLITPPYGASGY 62
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 NOKFRGKATLTVDKSSSTAYMDLISLTSBDSAIVFCARGYDGR--GFDYWGQGTTVTVS 119
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 NOKFRGKATLTVDKSSSTAYMDLISLTSBDSAIVFCARGYDGR--GFDYWGQGTTVTVS 121
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 SGVGGSGGGGSGGGSDIELTQSPALMSASPG 151
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 SGGGGSGGGGSGGGSE-----SSSPG 144
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
Q7TMK1

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ID Q7TMK1 PRELIMINARY; PRT; 470 AA.
AC Q7TMK1;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein A1324046.
GN Name=A1324046;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marnett L., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Mair M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055910; AAH55910.1; -.
DR HSSP; P01865; IKB5.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; CI-sec; 3.
DR SMART; SM00406; IGV, 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51727 MW; 6D90E4DF696B090 CRC64;

Query Match 40.3%; Score 514.5; DB 2; Length 470;
Best Local Similarity 52.1%; Pred. No. 3.8e-30;
Matches 122; Conservative 19; Mismatches 46; Indels 47; Gaps 8;

QY 2 QVLOOOSPELEKPGASVYLSCASGYSFTGYTMNWKSHGKSLKLEWIGLITPPYGASGY 61
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EVOLQOSPELVYKRGASVYLSCASGYSFTGYTMNWKSHGKSLKLEWIGLVNPNNGDSY 79
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 NOKFRGKATLTVDKSSSTAYMDLISLTSBDSAIVFCARGYDGR--GFDYWGQGTTVTVS 119
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NOKFRGKATLTVDKSSSTAYMDLISLTSBDSAIVFCARGYDGR--GFDYWGQGTTVTVS 139
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 SGVGGSGGGGSGGGSDIELTQSPALMSASP-----GEKTYMTCSASSSVSYHWYQOK 173
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 140 SAT-----TTASVYPIVNGCCDPTGSSVTLGCLV----- 169
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 174 SGTSPK---RWIYDTSKLASGVPGRFSGSGNSYSLTISSEAEADATYYCQ 223
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 170 KGYPPEPVYKWN--GALSSGVRTVSSVLSQSG--SSLVTVPSSTWPSQ 218
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

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RESULT 12
ID 06PUA7 PRELIMINARY; PRT; 472 AA.
AC 06PUA7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE .05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Muzny D.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
Villalón D.K., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
Krzyszinski M.I., Skalska U., Smalins D.E., Schermer A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018535; AAH18535.1; -.
DR HSSP; P01865; 1KB5.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_1.
DR InterPro; IPR003066; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-sect; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ
SEQUENCE 472 AA; 52299 MW; 165169C23D55D4AB CRC64;

Query Match 39.4%; Score 502.5; DB 2; Length 472;
Best Local Similarity 46.1%; Pred. No. 3e-29;
Matches 118; Conservative 26; Mismatches 59; Indels 53; Gaps 9;

QY 2 QVQLQSGPELTKPGASVSKLSCRASGYSTGYTMNWKQSHGKSLKLEWIGITPYNGASVY 61
DB 20 EVQLQSGPELVKTKGASVKMSCKRSGYTFSDYYHWKQSHGKSLKLEWIGITPYNGNGY 79
QY 62 NQKFRGKATLTVDKSSSTAYMDLISLTSEDSAVYFCARG-----GYRGKPDYWGQTTV 116
DB 80 NQKFRGKATLTVDKSSSTAYMDLISLTSEDSAVYFCARGISYYSYD-HYFDYWGQTTI 138
QY 117 TVSSGKVGSGSGGSGGSGSIEILQSPAIMSASP-----GEKVTMCSASSSYVMHWY 170
DB 139 TVSSA-----KTTAPSVYPLAVCGDPTGSSVTLGLVYK---GYF--- 175
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QY 171 QOKSGTSPKRWIYDTSKLASGVPRFSGSGSNYSLTISVEADDAITYYCOQMSGYPL 230
DB 176 -----PEPYTLTNMGSSLSGGV-HTFPAVLQSDLYTLSS-----VYTSSTWPSQSI 222
QY 231 TF-----GAGTKLEIK 241
DB 223 TCVVAHPASSTIVDKK 238

RESULT 13
ID 08K1FO PRELIMINARY; PRT; 112 AA.
AC 08K1FO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-Vipase light chain variable region (Fragment).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C; TISSUE=Hyperimmunized spleen;
RA Zhou Y.-X., Taguchi H., Planque S., Karle S., Nishiyama Y., Paul S.;
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516285; AAM64203.1; -.
DR PIR; A33933; A33933.
DR PIR; PC4405; PC4405.
DR HSSP; P01837; 1OR0.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 112
SQ
SEQUENCE 112 AA; 11901 MW; F6644663201AA239 CRC64;

Query Match 38.9%; Score 496; DB 2; Length 112;
Best Local Similarity 92.2%; Pred. No. 1.8e-29;
Matches 95; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 139 LTQSPAIMSAPGEKVTMTCSASSSYVMHWYQOKSGTSPKRWIYDTSKLASGVPRFSG 198
DB 4 LTQSPAIMSAPGEKVTMTCSASSSYVMHWYQOKSGTSPKRWIYDTSKLASGVPRFSG 63
QY 199 SSGNSYSLTISVEADDAITYYCOQMSGYPLTFGAGTKLEIK 241
DB 64 SSGNSYSLTISVEADDAITYYCOQMSNPPTFGGKLEIK 106

RESULT 14
ID 091WR1 PRELIMINARY; PRT; 488 AA.
AC 091WR1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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OM protein - protein search, using sw model

Run on: October 24, 2005, 18:46:59 : Search time 42 Seconds
(without alignments)
428.343 Million cell updates/sec

Title: US-09-979-539-1

Perfect score: 1276

Sequence: 1 MGVUQSGPELEKRGASVK.....CQWNGYPTFGATKLEIK 241

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/PCUS_COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1274	99.8	241	4	US-09-581-345-5 Sequence 5, Appl
2	993	77.8	244	2	US-08-553-497A-20 Sequence 20, Appl
3	987	77.4	242	2	US-08-553-497A-26 Sequence 26, Appl
4	982.5	77.0	297	4	US-09-486-814A-2 Sequence 2, Appl
5	981.5	76.9	599	1	US-08-463-163-3 Sequence 22, Appl
6	979	76.7	244	2	US-08-553-497A-22 Sequence 2, Appl
7	977	76.6	242	2	US-08-553-497A-28 Sequence 28, Appl
8	976.5	76.5	239	3	US-08-279-772A-8 Sequence 8, Appl
9	976.5	76.5	239	3	US-08-802-486-11 Sequence 11, Appl
10	972	76.2	246	2	US-08-553-497A-24 Sequence 24, Appl
11	959.5	75.2	256	4	US-09-526-738A-2 Sequence 2, Appl
12	959.5	75.2	258	4	US-09-526-738A-4 Sequence 4, Appl
13	956.5	75.0	495	4	US-09-948-004-18 Sequence 18, Appl
14	908	71.2	238	4	US-09-798-689-21 Sequence 21, Appl
15	902.5	70.7	246	2	US-08-469-486-57 Sequence 57, Appl
16	902.5	70.7	246	2	US-08-469-658-57 Sequence 57, Appl
17	889.5	69.7	270	2	US-08-652-507-2 Sequence 2, Appl
18	885.5	69.4	281	3	US-09-423-439-44 Sequence 44, Appl
19	885.5	69.4	666	3	US-09-423-439-51 Sequence 51, Appl
20	883.5	69.2	553	2	US-08-661-052-16 Sequence 16, Appl
21	883.5	69.2	553	3	US-09-188-082-16 Sequence 16, Appl
22	883.5	69.2	553	3	US-09-364-088-16 Sequence 16, Appl
23	883.5	69.2	553	3	US-09-102-716-16 Sequence 16, Appl
24	866	67.9	267	3	US-09-485-737B-2 Sequence 2, Appl
25	866	67.9	267	4	US-10-071-485-2 Sequence 2, Appl
26	866	67.9	541	3	US-09-485-737B-85 Sequence 85, Appl
27	866	67.9	541	4	US-10-071-485-85 Sequence 85, Appl

28	866	67.9	711	3	US-09-485-737B-90	Sequence 90, Appl
29	866	67.9	711	4	US-10-071-485-90	Sequence 90, Appl
30	854	66.9	284	3	US-09-184-658-40	Sequence 40, Appl
31	854	66.9	284	4	US-09-504-262D-40	Sequence 40, Appl
32	849.5	66.6	255	3	US-09-553-498-8	Sequence 8, Appl
33	849.5	66.6	255	4	US-09-618-869-8	Sequence 8, Appl
34	841.5	65.9	273	2	US-08-403-869-18	Sequence 18, Appl
35	841	65.9	235	2	US-08-190-199A-61	Sequence 61, Appl
36	839	65.8	267	4	US-09-419-788-30	Sequence 30, Appl
37	834.5	65.4	240	3	US-09-485-737B-91	Sequence 91, Appl
38	834.5	65.4	240	4	US-10-071-485-91	Sequence 91, Appl
39	831.5	65.2	240	2	US-08-800-198-8	Sequence 8, Appl
40	831.5	65.2	240	3	US-09-296-595-8	Sequence 8, Appl
41	829	65.0	288	3	US-09-423-439-38	Sequence 38, Appl
42	829	65.0	673	3	US-09-423-439-32	Sequence 32, Appl
43	823	64.5	260	2	US-08-447-402-1	Sequence 1, Appl
44	822.5	64.5	236	2	US-08-190-199A-65	Sequence 65, Appl
45	822	64.4	249	2	US-08-797-689-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-581-345-5

Sequence 5, Application US/09581345

Patent No. 6809184

GENERAL INFORMATION:

APPLICANT: Pastan, Ira H.

APPLICANT: Chowdhury, Patsha S.

APPLICANT: The Government of the United States

APPLICANT: as represented by the Secretary of the

Department of Health and Human Services

TITLE OF INVENTION: Antibodies, including Fv Molecules, and

TITLE OF INVENTION: Immunocjugates Having High Binding Affinity for

FILE REFERENCE: 015280-339100US

CURRENT APPLICATION NUMBER: US/09/581,345

CURRENT FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US 60/067,175

PRIOR FILING DATE: 1997-12-01

PRIOR APPLICATION NUMBER: WO PCT/US98/25270

PRIOR FILING DATE: 1998-11-25

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 5

LENGTH: 241

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:SS scFv

US-09-581-345-5

Query Match 99.8%: Score 1274; DB 4; Length 241;

Best Local Similarity 99.6%: Pred. No. 2.4e-95;

Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGVUQSGPELEKRGASVKSCKASGYFTGYTMNWVKQSHGKLEWIGLITPNQASS	60
DB	1	MGVUQSGPELEKRGASVKISCKASGYFTGYTMNWVKQSHGKLEWIGLITPNQASS	60
QY	61	YNQKRGKATLTVDKSSSTAYWDLSTLSBDAVYFCARAGYDGGFDYWGQGTIVYSS	120
DB	61	YNQKRGKATLTVDKSSSTAYWDLSTLSBDAVYFCARAGYDGGFDYWGQGTIVYSS	120
QY	121	GVGSGGGGSGGGSDIELTQSPAIMSAPGKVTMTCSASSSVSMYHVOQKSGTSPKR	180
DB	121	GVGSGGGGSGGGSDIELTQSPAIMSAPGKVTMTCSASSSVSMYHVOQKSGTSPKR	180
QY	181	WIYDTSKLASGYPGHFFSGSGSGNSYSLTISVEAEDATYYCQWNGYPTFGAGTKLEI	240
DB	181	WIYDTSKLASGYPGHFFSGSGSGNSYSLTISVEAEDATYYCQWNGYPTFGAGTKLEI	240

LENGTH: 242 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-497A-28

Query Match 76.6%; Score 977; DB 2; Length 242;

Best Local Similarity 78.1%; Pred. No. 2.2e-71;
Matches 189; Conservative 19; Mismatches 32; Indels 2; Gaps 1;

QY 2 QVQLQSGPELEKPKASVYKLSCKAGYSFTGYTMNWKSHGKSLIEWIGLITPPYNGASSY 61
Db 1 EVKLQSGAEIAYKPKASVYKLSCKAGSYFTTSHLDHWKQKQGLIEWIGLITPPYNGASSY 60
QY 62 NQKFRGKATLTVDKSSSTAYMDLSLTSEDSAVYFCARG--GYDRGPDYWGQGTIVTVSS 119
Db 61 NEKFSKATLTVDKSSSTAYIELSLTSEDCVYICASRDYDGRYDYPWGQGTIVTVSS 120
QY 120 SGVGGSGGGGGGGSDIELTQSPAIMSASPEKVTMTCSASSSVSYMHVYQKSGTSPK 179
Db 121 SGGGSGGGGGGGSDIELTQSPAIMSASPEKVTMTCSASSSVSYMHVYQKSGTSPK 180
QY 180 RMIYTSKLASGVPRFSGSGNSYSLTISVVEADDATYTCQWMSGYPLTFGAGTKLE 239
Db 181 LIYPTSNLASGVPRFSGSGTSTSLTISRMEADATYTCQWMSGYPLTFGAGTKLE 240
QY 240 IK 241
Db 241 IK 242

RESULT 8

US-08-279-772A-8
Sequence 8, Application US/08279772A

Patent No. 6080560

GENERAL INFORMATION:

APPLICANT: Russel1, David R

APPLICANT: Fuller, James T

TITLE OF INVENTION: Method for Producing Antibodies in Plant

TITLE OF INVENTION: Cells

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles and Brady

STREET: PO Box 2113

CITY: Madison

STATE: WI

COUNTRY: United States of America

ZIP: 53701-2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/279,772A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27,386

REFERENCE/DOCKET NUMBER: 11-229-9097-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-251-5000

TELEFAX: 608-251-9166

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 239 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-279-772A-8

Query Match 76.5%; Score 976.5; DB 3; Length 239;

Best Local Similarity 78.8%; Pred. No. 2.4e-71;
Matches 189; Conservative 14; Mismatches 34; Indels 3; Gaps 1;

QY 2 QVQLQSGPELEKPKASVYKLSCKAGYSFTGYTMNWKSHGKSLIEWIGLITPPYNGASSY 61
Db 3 QVQLQSGAEIAYKPKASVYKLSCKAGSYFTTSHLDHWKQKQGLIEWIGLITPPYNGASSY 62
QY 62 NQKFRGKATLTVDKSSSTAYMDLSLTSEDSAVYFCARGYDGRGPDYWGQGTIVTVSSG 121
Db 63 NQKFRGKATLTVDKSSSTAYMDLSLTSEDSAVYFCARGYDGRGPDYWGQGTIVTVSSG 119
QY 122 VGGSGGGGGGGGGSDIELTQSPAIMSASPEKVTMTCSASSSVSYMHVYQKSGTSPKRW 181
Db 120 GGGSGGGGGGGGGSDIELTQSPAIMSASPEKVTMTCSASSSVSYMHVYQKSGTSPKRW 179
QY 182 IYDTSKLASGVPRFSGSGNSYSLTISVVEADDATYTCQWMSGYPLTFGAGTKLEIK 241
Db 180 IYTSNLSASGVPRFSGSGTSTSLTISRMEADATYTCQWMSGYPLTFGAGTKLEIK 239

RESULT 9

US-08-902-486-11

Sequence 11, Application US/08902486

Patent No. 6140075

GENERAL INFORMATION:

APPLICANT: Russel, David R.

APPLICANT: Fuller, James T.

TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND

TITLE OF INVENTION: PROTEIN TOXINS IN PLANT CELLS

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady

STREET: 1 South Pinckney Street

CITY: Madison

STATE: WI

COUNTRY: US

ZIP: 53701-2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/902,486

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27386

REFERENCE/DOCKET NUMBER: 670513.90261

TELECOMMUNICATION INFORMATION:

TELEPHONE: 608-251-5000

TELEFAX: 608-251-9166

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 239 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-902-486-11

Query Match 76.5%; Score 976.5; DB 3; Length 239;

Best Local Similarity 78.8%; Pred. No. 2.4e-71;

Matches 189; Conservative 14; Mismatches 34; Indels 3; Gaps 1;

QY 2 QVQLQSGPELEKPKASVYKLSCKAGYSFTGYTMNWKSHGKSLIEWIGLITPPYNGASSY 61
Db 3 QVQLQSGAEIAYKPKASVYKLSCKAGSYFTTSHLDHWKQKQGLIEWIGLITPPYNGASSY 62
QY 62 NQKFRGKATLTVDKSSSTAYMDLSLTSEDSAVYFCARGYDGRGPDYWGQGTIVTVSSG 121
Db 63 NQKFRGKATLTVDKSSSTAYMDLSLTSEDSAVYFCARGYDGRGPDYWGQGTIVTVSSG 119

Qy	122	VGGSGGGGGGGGGSDIELTQSPAIMSASGEVYMTGCASSSVSPMHYQOKSGTSPRW	181
Db	120	GGSGGGGGGGGGGSGQVLVLPSPAIMSASGEKVTITTCASSSISMHFQCKPPTSPRLW	179
Qy	182	LYDTSLKASGVPCRFEGSGSSGNSYSYLTISVSVAEDADATYYCQMSGYPLTGTAGTKLEIK	241
Db	180	IYTTSMASGVPPARFEGSGSGTYSYLTISRMAEDAAATYYCHQRTYPLTGTSGTKLEIK	239

RESULT 10 497A-24
 : Sequence 24, Application US/08553497A
 : Patent No 5844093
 :
 : GENERAL INFORMATION:
 : APPLICANT: KETLEBOROUGH, C. A.
 : APPLICANT: BENDIG, MARY M.
 : APPLICANT: ANSELMI, KEITH H.
 : APPLICANT: GUSSOW, DETLEF
 : APPLICANT: ADAM, JAUME
 : APPLICANT: MTTIANS, FRANSSEC
 : APPLICANT: ROSELL, ELISABET
 : APPLICANT: BLASCO, FRANCESC
 : APPLICANT: PULANS, JAUME
 : TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
 : TITLE OF INVENTION: ANTIBODIES
 : NUMBER OF SEQUENCES: 30
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSER: MILLEN, WHITE, ZELANO & BRANIGAN, P. C.
 : STREET: 2200 CLARENDON BLVD. SUITE 1400
 : CITY: ARLINGTON
 : STATE: VA
 : COUNTRY: US
 : ZIP: 22201
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 :
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/553,497A
 : FILING DATE: 17-NOV-1995
 : CLASSIFICATION: 530
 :
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: WO PCT/EP95/00978
 : FILING DATE: 16-MAR-1995
 :
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: EP 94104160.0
 : FILING DATE: 17-MAR-1994
 :
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: EP 94118970.6
 : FILING DATE: 02-DEC-1994
 : ATTORNEY/AGENT INFORMATION:
 : NAME: HAMLET-KING, DIANA
 : REGISTRATION NUMBER: 33,302
 : REFERENCE/DOCKET NUMBER: MERCK 1726
 :
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 703-243-6333
 : TELEFAX: 703-243-6410
 :
 : INFORMATION FOR SEQ ID NO: 24:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 246 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 :
 : MOLECULE TYPE: protein
 :
 : US-08-553-497A-24

	Query Match	76.2%	Score	972;	DB 2;	Length	246;	
	Best Local Similarity	78.5%	Pred. No.	5, 7e-71;				
	Matches	193;	Conservative	14;	Mismatches	33;	Gaps	3
Oy	2 QVOTQSGPELEKPCASAYLSCSKAGCYFTGTMMVKQHCKSLSEWGLITPYNGASY	61						
Dh	1 EVOLQQSAAELVKKPASAVLSCKAAGYFTSTIMHVMKORAOQLGEMWGEFNSGRNTY	60						

[illegible]

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RESULT 11
US-09-526-738A-2
: Sequence 2, Application US/09526738A
: Patent No. 6630584
: GENERAL INFORMATION:
: APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT
: APPLICANT: LTD.
: TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
: FILE REFERENCE: 1196336
: CURRENT APPLICATION NUMBER: US/09/526, 738A
: CURRENT FILING DATE: 2000-03-16
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 2
: LENGTH: 256
: TYPE: PRT
: ORGANISM: Humans
: US-09-526-738A-2

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Query Match	75.2%;	Score 959.5;	DB 4;	Length 256;
Best Local Similarity	-77.6%;	Pred. No. 6.1e-70;		
Matches 187;	Conservative 13;	Mismatches 36;	Indels 5;	Gaps 2

[illegible]

RESULT 12 738A-4
US-09-526-738A-4
Sequence 4, Application US/09526738A
Patent No. 6630584
GENERAL INFORMATION:
APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT
APPLICANT: LTD.
TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
FILE REFERENCE: 1196336
CURRENT APPLICATION NUMBER: US/09/526, 738A
CURRENT FILING DATE: 2000-03-16

NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 258
TYPE: PRT
ORGANISM: Humanus
US-09-526-738A-4

Query Match 75.2%; Score 959.5; DB 4; Length 258;
Best Local Similarity 77.6%; Pred. No. 6,2e-70;
Matches 187; Conservative 13; Mismatches 36; Indels 5; Gaps 2;

QY 2 QVQLQSGPELEKPGASVYKLSCKASGYFTGYTMNWKSHKSLKLEWIGLTPPYNGASSY 61
DB 3 QVQLQSGPELEKPGASVYKLSCKASGYFTGYTMNWKSHKSLKLEWIGLTPPYNGASSY 62
QY 62 NQKFRKATLTVDKSSSTAYMDLSTLSEDSAVYFCARG-GYDGRGPDYWGQGTIVVSS 120
DB 63 NQKFRKATLTVDKSSSTAYMDLSTLSEDSAVYFCARG-GYDGRGPDYWGQGTIVVSS 118
QY 121 GVGSGGGGGGGGSDIELTQSPALMSASPEKVTMTCSASSSVYMHYQOKSGTSPKR 180
DB 119 GGGSGGGGGGGGSDIELTQSPALMSASPEKVTMTCSASSSVYMHYQOKSGTSPKR 178
QY 181 WYDTSKLASGVPRFSGSGSGNSYSLTISVVEAEDDATYTCQOMSGYPLTFGAGTKLEI 240
DB 179 WISSTSLASGVPRFSGSGSGNSYSLTISVVEAEDDATYTCQOMSGYPLTFGAGTKLEI 238
QY 241 K 241
DB 239 K 239

RESULT 13
US-09-948-004-18
Sequence 18, Application US/09948004
Patent No. 6723538

GENERAL INFORMATION:
APPLICANT: MACK, Mathias
TITLE OF INVENTION: Antibody and/or chemokine constructs and their use in
FILE REFERENCE: E 2411 EP
CURRENT APPLICATION NUMBER: US/09/948,004
CURRENT FILING DATE: 2001-09-05
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 495
TYPE: PRT
ORGANISM: Mus sp.
US-09-948-004-18

Query Match 75.0%; Score 956.5; DB 4; Length 495;
Best Local Similarity 76.9%; Pred. No. 2,4e-69;
Matches 186; Conservative 17; Mismatches 36; Indels 3; Gaps 1;

QY 3 VQLQSGPELEKPGASVYKLSCKASGYFTGYTMNWKSHKSLKLEWIGLTPPYNGASSY 62
DB 248 IKLQSGAEELARPGASVYKLSCKASGYFTGYTMNWKSHKSLKLEWIGLTPPYNGASSY 307
QY 63 OKFRKATLTVDKSSSTAYMDLSTLSEDSAVYFCARGYDGRGPDYWGQGTIVVSS-- 120
DB 308 OKFRKATLTVDKSSSTAYMDLSTLSEDSAVYFCARGYDGRGPDYWGQGTIVVSS-- 367
QY 121 -GVGSGGGGGGGGSDIELTQSPALMSASPEKVTMTCSASSSVYMHYQOKSGTSPK 179
DB 368 GGGSGGGGGGGGSDIELTQSPALMSASPEKVTMTCSASSSVYMHYQOKSGTSPK 427
QY 180 WYDTSKLASGVPRFSGSGSGNSYSLTISVVEAEDDATYTCQOMSGYPLTFGAGTKLE 239
DB 428 WYDTSKLASGVPRFSGSGSGNSYSLTISVVEAEDDATYTCQOMSGYPLTFGAGTKLE 487
QY 240 IK 241

DB 488 LK 489

RESULT 14
US-09-798-689-21
Sequence 21, Application US/09798689
Patent No. 6811779

GENERAL INFORMATION:
APPLICANT: Rockwell, Patricia
TITLE OF INVENTION: Method for Reducing Tumor Growth with VEGF Antagonists
FILE REFERENCE: Sequence Listings 1-41 for 381-25 CIP
Patent No. 6811779

QY 62 NQKFRKATLTVDKSSSTAYMDLSTLSEDSAVYFCAR--GYDGRGPDYWGQGTIVVSS 119
DB 61 NQKFRKATLTVDKSSSTAYMDLSTLSEDSAVYFCAR--GYDGRGPDYWGQGTIVVSS 116
QY 120 GVGSGGGGGGGGSDIELTQSPALMSASPEKVTMTCSASSSVYMHYQOKSGTSPK 179
DB 117 GGGSGGGGGGGGSDIELTQSPALMSASPEKVTMTCSASSSVYMHYQOKSGTSPK 176
QY 180 WYDTSKLASGVPRFSGSGSGNSYSLTISVVEAEDDATYTCQOMSGYPLTFGAGTKLE 239
DB 177 WYDTSKLASGVPRFSGSGSGNSYSLTISVVEAEDDATYTCQOMSGYPLTFGAGTKLE 236
QY 240 IK 241
DB 237 IK 238

RESULT 15
US-08-469-486-57
Sequence 57, Application US/08469486
Patent No. 5739281

GENERAL INFORMATION:
APPLICANT: Theegreen, Hans Christian
TITLE OF INVENTION: Improved method for the refolding of
NUMBER OF SEQUENCES: 58
Query Match 71.2%; Score 908; DB 4; Length 238;
Best Local Similarity 74.0%; Pred. No. 8,1e-66;
Matches 179; Conservative 17; Mismatches 40; Indels 6; Gaps 2;

/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version
/ SOFTWARE: #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/469,486
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/192,060
/ FILING DATE: February 4, 1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Paul T. Clark
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 06363/002001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617 542 5070
/ TELEFAX: 617 542 8906
/ TELEX: 200154
/ INFORMATION FOR SEQ. ID NO: 57:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 246 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-469-486-57

Query Match 70.7%; Score 902.5; DB 1; Length 246;
Best Local Similarity 73.9%; Pred. No. 2.3e-65;
Matches 178; Conservative 15; Mismatches 37; Indels 11; Gaps 2;

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|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 1 QVQLQSGALVLPQASVVKMSCKASGYTFASWINWVKORPGGLEWIGHIYFVRSITKY 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
QY 62 NQKFRKATLVVDKSSSTAYMDLISLTSEDSAVYFCARG-GYDGRGFDYWGGTTVVS8 120
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 61 NEKFKKATITLDTSSSTAYMQLSLTSEDSAVYYCSRGDSPDYAMDYWGQTTVVS- 119
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
QY 121 GVGGSGGGSGGGSDIELTQSPALMSASPGKRYVTMTCSASSSVSYMHWTQKSGTSPKR 180
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 120 -----SGGGSDIELTQSPALMSASPGKRYVTMTCSASSSVSYMHWTQKSGSPKR 170
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
QY 181 WIVDTSKLASGVPRFGSGSGNSYSITSSVEAEDATYYCOOWSGYPLTFAGTKLEI 240
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 171 WIVATSNLASGVPRFSGTSGTSLTISRVEAEDATYYCOOWSNPPTFGSGTKLEI 230
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
QY 241 K 241
|
Db 231 K 231

Search completed: October 24, 2005, 20:07:21
Job time : 44 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 24, 2005, 20:05:55 : Search time 165 Seconds
(without alignments)
609.812 Million cell updates/sec

Title: US-09-979-539-1
Perfect score: 1276
Sequence: 1 MQVQLQSGPHELEKRGASVK.....CQWNGYPLTFAGTKLEIK 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1862986 seqs, 417506248 residues

Total number of hits satisfying chosen parameters: 1862986

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1274	99.8	241	18	US-10-973-718-5
2	1025.5	80.4	242	14	US-10-259-087A-20
3	1025.5	80.4	242	16	US-10-689-006-20
4	1010.5	79.2	239	9	US-09-808-037-6
5	1010.5	79.2	239	14	US-10-162-889-6
6	1010.5	79.2	239	15	US-10-384-788-6
7	1010.5	79.2	239	15	US-10-618-856-6
8	1010.5	79.2	239	17	US-10-749-522-6
9	1010.5	79.2	239	20	US-11-073-526-6
10	1003	78.6	261	16	US-10-689-006-24
11	989.5	77.5	242	14	US-10-255-087A-18

12	989.5	77.5	242	16	US-10-689-006-18	Sequence 18, Appl
13	967.5	75.8	492	16	US-10-682-845-63	Sequence 63, Appl
14	967.5	75.8	492	16	US-10-682-845-79	Sequence 79, Appl
15	967.5	75.8	492	16	US-10-682-845-83	Sequence 83, Appl
16	966.5	75.7	492	16	US-10-682-845-87	Sequence 87, Appl
17	966	75.7	246	17	US-10-861-617-15	Sequence 15, Appl
18	965.5	75.7	492	16	US-10-682-845-61	Sequence 61, Appl
19	965.5	75.7	492	16	US-10-682-845-71	Sequence 71, Appl
20	965.5	75.7	492	16	US-10-682-845-73	Sequence 73, Appl
21	965.5	75.7	492	16	US-10-682-845-77	Sequence 77, Appl
22	964.5	75.6	243	18	US-10-966-406-2	Sequence 2, Appl1
23	964.5	75.6	409	15	US-10-362-591-2	Sequence 2, Appl1
24	964.5	75.6	492	16	US-10-682-845-59	Sequence 59, Appl
25	964.5	75.6	492	16	US-10-682-845-67	Sequence 67, Appl
26	964.5	75.6	492	16	US-10-682-845-69	Sequence 69, Appl
27	964.5	75.6	499	17	US-10-805-177-111	Sequence 111, App
28	964.5	75.6	500	14	US-10-168-809-22	Sequence 22, Appl
29	963.5	75.5	492	16	US-10-682-845-75	Sequence 75, Appl
30	963.5	75.5	492	16	US-10-682-845-85	Sequence 85, Appl
31	962.5	75.4	260	15	US-10-435-614-20	Sequence 20, Appl
32	961	75.3	246	17	US-10-861-617-17	Sequence 17, Appl
33	961	75.3	657	16	US-10-723-003-48	Sequence 48, Appl
34	960.5	75.3	492	16	US-10-682-845-65	Sequence 65, Appl
35	959.5	75.2	256	14	US-10-247-488-2	Sequence 2, Appl1
36	959.5	75.2	258	14	US-10-247-488-4	Sequence 4, Appl1
37	957.5	75.0	492	16	US-10-682-845-81	Sequence 81, Appl
38	956.5	75.0	495	10	US-09-948-004-18	Sequence 18, Appl
39	956.5	75.0	495	18	US-10-672-932-18	Sequence 18, Appl
40	956	74.9	281	14	US-10-112-788-9	Sequence 9, Appl1
41	956	74.9	281	15	US-10-435-614-15	Sequence 15, Appl
42	950	74.5	438	14	US-10-244-821-88	Sequence 88, Appl
43	948.5	74.3	260	15	US-10-435-614-19	Sequence 19, Appl
44	941.5	73.8	423	14	US/10/013	Sequence 8, Appl
45	941.5	73.8	423	14	US/10/150	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-10-973-718-5
Sequence 5, Application US/10973718
Publication No. US20050214304A1
GENERAL INFORMATION:
APPLICANT: Pastan, Ira H.
APPLICANT: Chowdhury, Partha S.
APPLICANT: The Government of the United States
APPLICANT: as represented by the Secretary of the
Department of Health and Human Services
TITLE OF INVENTION: Antibodies, including Fv Molecules, and
TITLE OF INVENTION: Immunconjugates Having High Binding Affinity for
FILE REFERENCE: 015280-339100US
CURRENT APPLICATION NUMBER: US/10/973,718
CURRENT FILING DATE: 2004-10-25
PRIOR APPLICATION NUMBER: US/09/581,345
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/067,175
PRIOR FILING DATE: 1997-12-01
PRIOR APPLICATION NUMBER: WO PCT/US98/25270
PRIOR FILING DATE: 1998-11-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 241
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:SS scfv
US-10-973-718-5
Query Match 99.8%; Score 1274; DB 18; Length 241;
Best Local Similarity 99.6%; Pred. No. 1.2e+02;

Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOVOLOOSGPELEKPGASVYLKSCASGYSTGYTMNMWVKSHGKSLMIGLITPYNGASS 60
Db 1 MOVOLOOSGPELEKPGASVYLKSCASGYSTGYTMNMWVKSHGKSLMIGLITPYNGASS 60

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Db 61 YNOKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGYDGRGPDYWGQGTTVVSS 120

QY 121 GVGSGGGGGGGGSDIELTQSPAIMSASPEKVTMTCSASSSVYMHWTQOKSGTSPKR 180
Db 121 GVGSGGGGGGGGSDIELTQSPAIMSASPEKVTMTCSASSSVYMHWTQOKSGTSPKR 180

QY 181 WIYDTSKLASGVPRFSGSGSNGNSYSLTSSVEAEDATYCCQWMSGYPLTFGAGTKLEI 240
Db 181 WIYDTSKLASGVPRFSGSGSNGNSYSLTSSVEAEDATYCCQWMSGYPLTFGAGTKLEI 240

QY 241 K 241
Db 241 K 241

RESULT 2

US-10-259-087A-20
; Sequence 20, Application US/10259087A
; Publication No. US20030130190A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; TITLE OF INVENTION: IN VIVO PANNING FOR LIGANDS TO RADIATION-INDUCED MOLECULES
; FILE REFERENCE: 1242/47/2
; CURRENT APPLICATION NUMBER: US/10/259, 087A
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/328123
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial antibody ligand number 2
US-10-259-087A-20

Query Match 80.4%; Score 1025.5; DB 14; Length 242;
Best Local Similarity 81.7%; Pred. No. 5.2e-65;
Matches 196; Conservative 13; Mismatches 30; Indels 1; Gaps 1;

QY 2 QVOLOOSGPELEKPGASVYLKSCASGYSTGYTMNMWVKSHGKSLMIGLITPYNGASSY 61
Db 3 QVOLOOSGPELEKPGASVYLKSCASGYSTGYTMNMWVKSHGKSLMIGLITPYNGASSY 62

QY 62 NOKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGYDGRGPDYWGQGTTVVSSG 121
Db 63 NOKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGYDGRGPDYWGQGTTVVSSG 121

QY 122 VGSAGGGGGGGGSDIELTQSPAIMSASPEKVTMTCSASSSVYMHWTQOKSGTSPKR 181
Db 122 VGSAGGGGGGGGSDIELTQSPAIMSASPEKVTMTCSASSSVYMHWTQOKSGTSPKR 181

QY 182 IYDTSKLASGVPRFSGSGSNGNSYSLTSSVEAEDATYCCQWMSGYPLTFGAGTKLEI 241
Db 182 IYDTSKLASGVPRFSGSGSNGNSYSLTSSVEAEDATYCCQWMSGYPLTFGAGTKLEI 241

RESULT 3

US-10-689-006-20
; Sequence 20, Application US/10689006
; Publication No. US20040191249A1
; GENERAL INFORMATION:

; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; APPLICANT: Mettenough, Raymond
; TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
; FILE REFERENCE: 1242/72
; CURRENT APPLICATION NUMBER: US/10/689, 006
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US 09/914,605
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 10/259,087
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial antibody ligand number 2
US-10-689-006-20

Query Match 80.4%; Score 1025.5; DB 16; Length 242;
Best Local Similarity 81.7%; Pred. No. 5.2e-65;
Matches 196; Conservative 13; Mismatches 30; Indels 1; Gaps 1;

QY 2 QVOLOOSGPELEKPGASVYLKSCASGYSTGYTMNMWVKSHGKSLMIGLITPYNGASSY 61
Db 3 QVOLOOSGPELEKPGASVYLKSCASGYSTGYTMNMWVKSHGKSLMIGLITPYNGASSY 62

QY 62 NOKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGYDGRGPDYWGQGTTVVSSG 121
Db 63 NOKFRGKATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGYDGRGPDYWGQGTTVVSSG 121

QY 122 VGSAGGGGGGGGSDIELTQSPAIMSASPEKVTMTCSASSSVYMHWTQOKSGTSPKR 181
Db 122 VGSAGGGGGGGGSDIELTQSPAIMSASPEKVTMTCSASSSVYMHWTQOKSGTSPKR 181

QY 182 IYDTSKLASGVPRFSGSGSNGNSYSLTSSVEAEDATYCCQWMSGYPLTFGAGTKLEI 241
Db 182 IYDTSKLASGVPRFSGSGSNGNSYSLTSSVEAEDATYCCQWMSGYPLTFGAGTKLEI 241

RESULT 4

US-09-808-037-6
; Sequence 6, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beki
; APPLICANT: HANAN, Eliat
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; FILE REFERENCE: SOLOMON=2D
; CURRENT APPLICATION NUMBER: US/09/808, 037
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/629, 971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-037-6

Query Match 79.2%; Score 1010.5; DB 9; Length 239;
Best Local Similarity 79.8%; Pred. No. 5.9e-64;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;

QY 2 QVOLOOSGPELEKPGASVYLKSCASGYSTGYTMNMWVKSHGKSLMIGLITPYNGASSY 61

```
Db      1  QVKLOESGAEIVRPGVSVKISCKSGGYFTDYAMHVMVKOSHAKSLEWIGVISTYGDASY 60
Qy      62  NOKFRKATLTVDKSSSTAYMDLLSTPDSAVYPCAR---GYDGRGPDYGGGTTTV 118
Db      61  NOKFRKATMTVDKSSSTAYMDLLSTPDSAVYPCAR---FDYWGQVTTTV 116
Qy      119  SSGVGGSGGSGGSDIELTQSPAIMSASPEKVTMTCSASSSVYMHYQOKSGTSP 178
Db      117  SSGGGGSGGSGGSDIELTQSPAIMSASPEKVTMTCSASSSVYMHYQOKRGTS 176
Qy      179  KRWIVDTSKLASGVPRFSGSGSGNSYSLTISSVEAEDDATYCCQWMSGYPLTFGAGT 238
Db      177  KRWIVDTSKLASGVPRFSGSGSGNSYSLTISSVEAEDDATYCCQWMSGYPLTFGAGT 236
Qy      239  EIK 241
Db      237  EIK 239
```

RESULT 5

```
US-10-162-889-6
; Sequence 6, Application US/10162889
; Publication No. US20030077252A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beke
; APPLICANT: HANAN, Elia
; TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME
; TITLE OF INVENTION: USEFUL IN DIAGNOSING
; FILE REFERENCE: AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES
; FILE REFERENCE: SOLOMON=2B
; CURRENT APPLICATION NUMBER: US/10/162,889
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US/09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-889-6
```

```
Query Match      79.2%; Score 1010.5; DB 14; Length 239;
Best Local Similarity 79.8%; Pred. No. 5.9e-64;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;
```

```
Qy      2  QVLOOQSGPELEKPGASVYKLSCKASGYFTGYTMNVKQSHKSLIEMIGLITPYNGASSY 61
Db      1  QVKLOESGAEIVRPGVSVKISCKSGGYFTDYAMHVMVKOSHAKSLEWIGVISTYGDASY 60
Qy      62  NOKFRKATLTVDKSSSTAYMDLLSTPDSAVYPCAR---GYDGRGPDYGGGTTTV 118
Db      61  NOKFRKATMTVDKSSSTAYMDLLSTPDSAVYPCAR---FDYWGQVTTTV 116
Qy      119  SSGVGGSGGSGGSDIELTQSPAIMSASPEKVTMTCSASSSVYMHYQOKSGTSP 178
Db      117  SSGGGGSGGSGGSDIELTQSPAIMSASPEKVTMTCSASSSVYMHYQOKRGTS 176
Qy      179  KRWIVDTSKLASGVPRFSGSGSGNSYSLTISSVEAEDDATYCCQWMSGYPLTFGAGT 238
Db      177  KRWIVDTSKLASGVPRFSGSGSGNSYSLTISSVEAEDDATYCCQWMSGYPLTFGAGT 236
Qy      239  EIK 241
Db      237  EIK 239
```

RESULT 6

```
US-10-384-788-6
; Sequence 6, Application US/10384788
; Publication No. US20040013647A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beke
; APPLICANT: FRENKEL, Dan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A PLAQUE-FORMING DISEASE
; FILE REFERENCE: SOLOMON=2D.2
; CURRENT APPLICATION NUMBER: US/10/384,788
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 60/371,735
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 09/808,037
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/830,954
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 10/162,889
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 60/152,417
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: PCT/IL00/00518
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-384-788-6
```

```
Query Match      79.2%; Score 1010.5; DB 15; Length 239;
Best Local Similarity 79.8%; Pred. No. 5.9e-64;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;
```

```
Qy      2  QVLOOQSGPELEKPGASVYKLSCKASGYFTGYTMNVKQSHKSLIEMIGLITPYNGASSY 61
Db      1  QVKLOESGAEIVRPGVSVKISCKSGGYFTDYAMHVMVKOSHAKSLEWIGVISTYGDASY 60
Qy      62  NOKFRKATLTVDKSSSTAYMDLLSTPDSAVYPCAR---GYDGRGPDYGGGTTTV 118
Db      61  NOKFRKATMTVDKSSSTAYMDLLSTPDSAVYPCAR---FDYWGQVTTTV 116
Qy      119  SSGVGGSGGSGGSDIELTQSPAIMSASPEKVTMTCSASSSVYMHYQOKSGTSP 178
Db      117  SSGGGGSGGSGGSDIELTQSPAIMSASPEKVTMTCSASSSVYMHYQOKRGTS 176
Qy      179  KRWIVDTSKLASGVPRFSGSGSGNSYSLTISSVEAEDDATYCCQWMSGYPLTFGAGT 238
Db      177  KRWIVDTSKLASGVPRFSGSGSGNSYSLTISSVEAEDDATYCCQWMSGYPLTFGAGT 236
Qy      239  EIK 241
Db      237  EIK 239
```

RESULT 7

```
US-10-618-856-6
; Sequence 6, Application US/10618856
; Publication No. US20040052766A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beke
; APPLICANT: FRENKEL, Dan
; TITLE OF INVENTION: IMMUNIZATION AGAINST AMYLOID PLAQUES USING DISPLAY TECHNOLOGY
; FILE REFERENCE: SOLOMON=2A
; CURRENT APPLICATION NUMBER: US/10/618,856
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/473,653A
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
```

;; PRIOR FILING DATE: 1999-09-03
;; NUMBER OF SEQ ID NOS: 26
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 6
;; LENGTH: 239
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-618-856-6

Query Match 79.2%; Score 1010.5; DB 15; Length 239;
Best Local Similarity 79.8%; Pred. No. 5.9e-64;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSTGYTMNWVKSHGKSLIEWIGLITPYNGASSY 61
DB 1 QVQLQSGPELEKPGASVKLSCKASGYSTGYTMNWVKSHGKSLIEWIGLITPYNGASSY 60
QY 62 NQKFRKATLTVDKSSSTAYMDLSTSEDAVYFCARG---GYDGRGPDYWGQTTVTV 118
DB 61 NQKFRKATLTVDKSSSTAYMDLSTSEDAVYFCARGTMSY---FDYWGQVTVTVV 116
QY 119 SSGVGSGGGGGSGGSDIELTQSPALMSASPEKVTMTCSASSSVYMHWYQOKSGTSP 178
DB 117 SSGGGSGGGVSGGGSDIELTQSPALMSASPEKVTMTCSASSSVYMHWYQOKSGTSP 176
QY 179 KRWIYDTSLKASGVPRFSGSGSNYSYLTISVVEAEDDATYTCQOWSGYPLTFGAGTKL 238
DB 177 KRWIYDTSLKASGVPRFSGSGSGTSLTISMEADATYTCQORSSYPTFFGGAKL 236
QY 239 EIK 241
DB 237 EIK 239

RESULT 8
US-10-749-522-6
; Sequence 6, Application US/10749522
; Publication No. US20050089510A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Bekka
; APPLICANT: HANAN, Elia
; TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME USEFUL IN DIAG
; FILE REFERENCE: SOLOMON=2B
; CURRENT APPLICATION NUMBER: US/10749,522
; PRIOR FILING DATE: 2004-01-02
; PRIOR APPLICATION NUMBER: US/09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-749-522-6

Query Match 79.2%; Score 1010.5; DB 17; Length 239;
Best Local Similarity 79.8%; Pred. No. 5.9e-64;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSTGYTMNWVKSHGKSLIEWIGLITPYNGASSY 61
DB 1 QVQLQSGPELEKPGASVKLSCKASGYSTGYTMNWVKSHGKSLIEWIGLITPYNGASSY 60
QY 62 NQKFRKATLTVDKSSSTAYMDLSTSEDAVYFCARG---GYDGRGPDYWGQTTVTV 118
DB 61 NQKFRKATLTVDKSSSTAYMDLSTSEDAVYFCARGTMSY---FDYWGQVTVTVV 116
QY 119 SSGVGSGGGGGSGGSDIELTQSPALMSASPEKVTMTCSASSSVYMHWYQOKSGTSP 178

DB 117 SSGGGSGGGVSGGGSDIELTQSPALMSASPEKVTMTCSASSSVYMHWYQOKSGTSP 176
QY 179 KRWIYDTSLKASGVPRFSGSGSNYSYLTISVVEAEDDATYTCQOWSGYPLTFGAGTKL 238
DB 177 KRWIYDTSLKASGVPRFSGSGSGTSLTISMEADATYTCQORSSYPTFFGGAKL 236
QY 239 EIK 241
DB 237 EIK 239

RESULT 9
US-11-073-526-6
; Sequence 6, Application US/11073526
; Publication No. US20050152878A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Bekka
; APPLICANT: FRENKEL, Dan
; APPLICANT: HANAN, Elia
; TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME USEFUL IN DIAG
; FILE REFERENCE: SOLOMON=2C
; CURRENT APPLICATION NUMBER: US/11/073,526
; PRIOR FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/09/830,954
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: PCT/IL00/00518
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-526-6

Query Match 79.2%; Score 1010.5; DB 20; Length 239;
Best Local Similarity 79.8%; Pred. No. 5.9e-64;
Matches 194; Conservative 16; Mismatches 26; Indels 7; Gaps 2;

QY 2 QVQLQSGPELEKPGASVKLSCKASGYSTGYTMNWVKSHGKSLIEWIGLITPYNGASSY 61
DB 1 QVQLQSGPELEKPGASVKLSCKASGYSTGYTMNWVKSHGKSLIEWIGLITPYNGASSY 60
QY 62 NQKFRKATLTVDKSSSTAYMDLSTSEDAVYFCARG---GYDGRGPDYWGQTTVTV 118
DB 61 NQKFRKATLTVDKSSSTAYMDLSTSEDAVYFCARGTMSY---FDYWGQVTVTVV 116
QY 119 SSGVGSGGGGGSGGSDIELTQSPALMSASPEKVTMTCSASSSVYMHWYQOKSGTSP 178
DB 117 SSGGGSGGGVSGGGSDIELTQSPALMSASPEKVTMTCSASSSVYMHWYQOKSGTSP 176
QY 179 KRWIYDTSLKASGVPRFSGSGSNYSYLTISVVEAEDDATYTCQOWSGYPLTFGAGTKL 238
DB 177 KRWIYDTSLKASGVPRFSGSGSGTSLTISMEADATYTCQORSSYPTFFGGAKL 236
QY 239 EIK 241
DB 237 EIK 239

RESULT 10
US-10-689-006-24
; Sequence 24, Application US/10689006
; Publication No. US20040191249A1
; GENERAL INFORMATION:

```

; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; APPLICANT: Mernaugh, Raymond
; TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
; FILE REFERENCE: 1242/72
; CURRENT APPLICATION NUMBER: US/10/689,006
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US 09/914,605
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 10/259,087
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 261
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: nucleic acid encoding scfv antibody 10A
US-10-689-006-24
```

```

Query Match          78.6%; Score 1003; DB 16; Length 261;
Best Local Similarity 80.4%; Pred. No. 2.2e-63;
Matches 195; Conservative 17; Mismatches 27; Indels 2; Gaps 2;
```

```

QY 2 OVQLQSGPELEKPGASVYKLSCKASGYFTGYTMVMVQSHGKSLIEWITGLITPNYGASSY 61
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QVKLQSGPELVKPGASVYKLSCKASGYFTGYTMVMVQSHGKSLIEWITGLITPNYGASSY 62
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 NQKFRGKATLTVDKSSSTAYMDLSTLSEDSAVYFCAR-GGYDGRGFDYWGQGTIVTVSS 120
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 NQKFRGKATLTVDKSSSTAYMDLSTLSEDSAVYFCARWDGYG-GFTWGGGTIVTVSS 121
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 GVGSGGGSGGGSDIELTQSPAIMSASPGKVTMTCSASSSVSYMHVYQKSGTSPKR 180
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 122 GGGSGGGSGGGSDIELTQSPAIMSATLGEKVTMCSASSSVSYMHVYQKSGASPRL 181
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 WYDTSKLASGVPRGFSGSGNSYSLTSSVEARDATYYCOQMSGYPLTGAQTKLEI 240
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 182 WYDTSKLASGVPRGFSGSGNSYSLTSSVEARDATYYCOQMSGYPLTGAQTKLEI 241
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 241 K 241
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 242 K 242
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```

RESULT 11
US-10-259-087A-18
; Sequence 18, Application US/10259087A
; Publication No. US20030130190A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; APPLICANT: Ou, Shihmian
; TITLE OF INVENTION: IN VIVO PANNING FOR LIGANDS TO RADIATION-INDUCED MOLECULES
; FILE REFERENCE: 1242/47/2
; CURRENT APPLICATION NUMBER: US/10/259,087A
; CURRENT FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/328123
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial antibody ligand number 1
US-10-259-087A-18
```

```

Query Match          77.5%; Score 989.5; DB 14; Length 242;
Best Local Similarity 80.4%; Pred. No. 1.9e-62;
Matches 193; Conservative 14; Mismatches 32; Indels 1; Gaps 1;
```

```

QY 2 OVQLQSGPELEKPGASVYKLSCKASGYFTGYTMVMVQSHGKSLIEWITGLITPNYGASSY 61
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QVKLQSGPELVKPGASVYKLSCKASGYFTGYTMVMVQSHGKSLIEWITGLITPNYGASSY 62
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 NQKFRGKATLTVDKSSSTAYMDLSTLSEDSAVYFCARGYDGRGFDYWGQGTIVTVSSG 121
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 NQKFRGKATLTVDESSSTAYMDLSTLSEDSAVYFCARGYYS-AFDYWGQGTIVTVSSG 121
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 122 VGGSGGGSGGGSDIELTQSPAIMSASPGKVTMTCSASSSVSYMHVYQKSGTSPKR 181
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 122 GGGSGGGSGGGSDIELTQSPITMAASPGKVTITCRASSSVSYMHVYQKSGTSPKR 181
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 182 IYDTSKLASGVPRGFSGSGNSYSLTSSVEARDATYYCOQMSGYPLTGAQTKLEI 241
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 182 IYDTSKLASGVPRGFSGSGNSYSLTSSVEARDATYYCLORSSPYPTFGAGTKLEIK 241
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```

RESULT 12
US-10-689-006-18
```

```

; Sequence 18, Application US/10689006
; Publication No. US20040191249A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Mernaugh, Raymond
; APPLICANT: Hallahan, Dennis E
; TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
; FILE REFERENCE: 1242/72
; CURRENT APPLICATION NUMBER: US/10/689,006
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US 09/914,605
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 10/259,087
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial antibody ligand number 1
US-10-689-006-18
```

```

Query Match          77.5%; Score 989.5; DB 16; Length 242;
Best Local Similarity 80.4%; Pred. No. 1.9e-62;
Matches 193; Conservative 14; Mismatches 32; Indels 1; Gaps 1;
```

```

QY 2 OVQLQSGPELEKPGASVYKLSCKASGYFTGYTMVMVQSHGKSLIEWITGLITPNYGASSY 61
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 QVKLQSGPELVKPGASVYKLSCKASGYFTGYTMVMVQSHGKSLIEWITGLITPNYGASSY 62
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 NQKFRGKATLTVDKSSSTAYMDLSTLSEDSAVYFCARGYDGRGFDYWGQGTIVTVSSG 121
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 NQKFRGKATLTVDESSSTAYMDLSTLSEDSAVYFCARGYYS-AFDYWGQGTIVTVSSG 121
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 122 VGGSGGGSGGGSDIELTQSPAIMSASPGKVTMTCSASSSVSYMHVYQKSGTSPKR 181
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 122 GGGSGGGSGGGSDIELTQSPITMAASPGKVTITCRASSSVSYMHVYQKSGTSPKR 181
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 182 IYDTSKLASGVPRGFSGSGNSYSLTSSVEARDATYYCOQMSGYPLTGAQTKLEI 241
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 182 IYDTSKLASGVPRGFSGSGNSYSLTSSVEARDATYYCLORSSPYPTFGAGTKLEIK 241
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```

RESULT 13
```

```

US-10-682-845-63
; Sequence 63, Application US/10682845
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; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
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; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EPCAMxCD3 with M4 mutant in anti-CD3 part
US-10-682-845-63
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Query Match          75.8%; Score 967.5; DB 16; Length 492;
Best Local Similarity 77.3%; Pred. No. 1,4e-60;
Matches 187; Conservative 17; Mismatches 35; Indels 3; Gaps 1;
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QY 3 VOLQSGPELEKPGASVYKSCASGYSFTGYTMWVKQSHGKSLIEWITGLITPYNGASSYN 62
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DB 245 IKLQSGAELARPGASVYKSCKTSGYTFRTYTMWVKORPGGLEWIGYINPSRGYNTYN 304
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QY 63 OKRKGATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTIVTYS-- 120
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DB 305 OKRKGATLTVDKSSSTAYMDLLSLTSEDSAVYFCARSDHXCDDYWGQGTITLVSSVE 364
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QY 121 -GVGSGGGGGGGGGSDIELTQSPAIMSASPEKVTMTCSASSSVSYMHWYQKSGTSPK 179
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 365 GGGSGGGGGGGGGGVDIQLTQSPAIMSASPEKVTMTCSASSSVSYMHWYQKSGTSPK 424
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 180 RWIYDTSKLASGYPRFGSGSGNSYSLTSSVEADDAATYYCOQWSGPIPLFGAGTKLE 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 425 RWIYDTSKLASGYPRFGSGSGNSYSLTSSVEADDAATYYCOQWSNPLIFGAGTKLE 484
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QY 240 IK 241
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DB 485 LK 486
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RESULT 14
US-10-682-845-79
; Sequence 79, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EPCAMxCD3 with M31 mutant in anti-CD3 part
US-10-682-845-79
```

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Query Match          75.8%; Score 967.5; DB 16; Length 492;
Best Local Similarity 77.8%; Pred. No. 1,4e-60;
Matches 189; Conservative 18; Mismatches 31; Indels 5; Gaps 3;
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QY 3 VOLQSGPELEKPGASVYKSCASGYSFTGYTMWVKQSHGKSLIEWITGLITPYNGASSYN 62
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DB 245 IKLQSGAELARPGASVYKSCKTSGYTFRTYTMWVKORPGGLEWIGYINPSRGYNTYN 304
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QY 63 OKRKGATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGR-GFDYWGQGTIVTYS- 120
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DB 305 OKRKGATLTVDKSSSTAYMDLLSLTSEDSAVYFCAR-YBERYCLDDYWGQGTITLVSSV 363
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 -GVGSGGGGGGGGGSDIELTQSPAIMSASPEKVTMTCSASSSVSYMHWYQKSGTSP 178
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DB 365 GGGSGGGGGGGGGGVDIQLTQSPAIMSASPEKVTMTCSASSSVSYMHWYQKSGTSP 423
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QY 179 KRWIYDTSKLASGYPRFGSGSGNSYSLTSSVEADDAATYYCOQWSGPIPLFGAGTKL 238
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 424 KRWIYDTSKLASGYPRFGSGSGNSYSLTSSVEADDAATYYCOQWSNPLIFGAGTKL 483
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DB 484 LK 486
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RESULT 15
US-10-682-845-83
; Sequence 83, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EPCAMxCD3 with M65 mutant in anti-CD3 part
US-10-682-845-83
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Query Match          75.8%; Score 967.5; DB 16; Length 492;
Best Local Similarity 77.3%; Pred. No. 1,4e-60;
Matches 187; Conservative 17; Mismatches 35; Indels 3; Gaps 1;
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QY 3 VOLQSGPELEKPGASVYKSCASGYSFTGYTMWVKQSHGKSLIEWITGLITPYNGASSYN 62
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DB 245 IKLQSGAELARPGASVYKSCKTSGYTFRTYTMWVKORPGGLEWIGYINPSRGYNTYN 304
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 63 OKRKGATLTVDKSSSTAYMDLLSLTSEDSAVYFCARGGYDGRGFDYWGQGTIVTYS-- 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 305 OKRKGATLTVDKSSSTAYMDLLSLTSEDSAVYFCARSDHXCDDYWGQGTITLVSSVE 364
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 -GVGSGGGGGGGGGSDIELTQSPAIMSASPEKVTMTCSASSSVSYMHWYQKSGTSPK 179
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 365 GGGSGGGGGGGGGGVDIQLTQSPAIMSASPEKVTMTCSASSSVSYMHWYQKSGTSPK 424
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 180 RWIYDTSKLASGYPRFGSGSGNSYSLTSSVEADDAATYYCOQWSGPIPLFGAGTKLE 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 425 RWIYDTSKLASGYPRFGSGSGNSYSLTSSVEADDAATYYCOQWSNPLIFGAGTKLE 484
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 240 IK 241
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DB 485 LK 486
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Search completed: October 24, 2005, 20:20:03
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